

AMENDMENTS TO THE SPECIFICATION

Please replace the paragraphs at page 6, lines 22-27 with the following rewritten paragraphs:

-- **Figures 7A-7H** show the cDNA sequence (SEQ ID NO: 19) and amino acid sequence (SEQ ID NO: 111) of Gene 454 with the corresponding SNPs underlined.

Figure 8 shows the results of RT-PCR analysis of Gene 561.1 and Gene 561.2.

Figures 9A-9F show the cDNA sequence (SEQ ID NO: 90) and amino acid sequence (SEQ ID NO: 153) of Gene 757 with the corresponding SNPs underlined. --

Please replace the paragraphs at page 9, lines 3-6 with the following rewritten paragraphs:

-- **Figures 27A-27K** show the cDNA sequence (SEQ ID NO: 30) and amino acid sequence (SEQ ID NO: 120) of Gene 561.1 with the corresponding SNPs underlined.

Figures 28A-28C show the cDNA sequence (SEQ ID NO: 32) and amino acid sequence (SEQ ID NO: 121) of Gene 561.2 with the corresponding SNPs underlined. --

Please replace line 21 at page 49 with the following rewritten line:

-- NO: 6160), GLU-GLU, and DYKDDDDK (SEQ ID NO: 4688) (FLAG®) epitope tags. --

Please replace Table 2 on pages 128-137 with the following table:

PLEASE SEE NEXT PAGE FOR TABLE

TABLE 2: PRIMER PAIRS

Marker name	Locus	DNA type	Gene	Forward primer	Seq ID NO.	Reverse primer	Seq ID NO.
B0610N03-A1 x		BACend		CAAGCGATAGTTCCTAATTTCT	<u>4689</u>	TATGTGTTGGAGCCAGAAAATT	<u>4714</u>
B0600D18-A2 x		BACend		TGGTGTCTCTGAGCTTCACAG	<u>4690</u>	ACCGAACCAAGATCTCGGAAG	<u>4715</u>
B0611O14-A2 x		BACend		GTCCTGATTTTAAAGTTTGAGG	<u>4691</u>	CTGCCCTCACCTTGCCCTCAAC	<u>4716</u>
B0700A09-A2 x		BACend		GCTGCTTCCAGCATTTTCAGCAT	<u>4692</u>	CAGTGTATATGTGATGCTGAA	<u>4717</u>
B0716I10-A2 x		BACend		ATGATGCAGTGAAGTGAACCCA	<u>4693</u>	CTTACTCAGTACACTGGGCTCTC	<u>4718</u>
B1118B13-A2 x		BACend		GCACGTGGGTCTTCTCATCTGCT	<u>4694</u>	ACTCTCGTGGATAGAGCAGATG	<u>4719</u>
B1128N10-A2 x		BACend		CACGAGAGTCTAGTGGGGGTTT	<u>4695</u>	TCACCTGGCAGATGAACCCCG	<u>4720</u>
B0841C17-A2 x		BACend		TCGCCCTGATATCCACTATCTTT	<u>4696</u>	CATTAGATGATGGTAAAGATAG	<u>4721</u>
B0904G06-A2 x		BACend		ACTGCTCATTTCTTTACAGAAA	<u>4697</u>	GGAACAGCAAAACGTTTTCTGTA	<u>4722</u>
B0923J13-A2 x		BACend		CAGGTCTCTGCAGAGCAATTTCT	<u>4698</u>	GACCTCTGTTAACGAGAAATGC	<u>4723</u>
B0675M15-A2 x		BACend		GCAGACAATATCAAGAGTTCTT	<u>4699</u>	CTGTAAACACATCTCAAGAACTC	<u>4724</u>
B0600D18-A2 y		BACend		TCATCTGCCAAGTGAGCCCAAGT	<u>4700</u>	GACCTACCCAAAGCACTGGGCT	<u>4725</u>
B0610N03-A2 y		BACend		GATACCAATGTGAAGTCTCTTGA	<u>4701</u>	GTTTTCTTCCAGCCTCAAGGAC	<u>4726</u>
B0700A09-A2 y		BACend		TCTCGATCCCACTAACCCAGCAT	<u>4702</u>	ATGAAGTACATTGGATGTTGTT	<u>4727</u>
B1118B13-A2 y		BACend		ACTGGAATGCTCAAGCTCGATGC	<u>4703</u>	TTCCTCAAGGGTCAAGCATCCAG	<u>4728</u>
B1128N10-A2 y		BACend		TGCTGATCTCTCAGTTACACCT	<u>4704</u>	GCAAGCCACCCATCAGGGTGAA	<u>4729</u>
B0904G06-A2 y		BACend		ATCTAATGCTGTGGCCCGCTGCT	<u>4705</u>	GGTTTGTGTTGCTGCAGCAGCGG	<u>4730</u>
B0923J13-A2 y		BACend		GACAGCCAGAGGAAACCTCTTTC	<u>4706</u>	AAAAGTTGTCTTGGGAAGAGGT	<u>4731</u>
B0675M15-A2 y		BACend		CACCTCTGGCTTTCTTACCAACC	<u>4707</u>	AGCTGTGACATGAAGGTTGTAG	<u>4732</u>
B0635H04-A1 x		BACend		AGCTTCGTCTGACCAAGTCTACC	<u>4708</u>	TTCAGGAACCAACCAAGTAGACT	<u>4733</u>
B0666B20-A1 x		BACend		TGCCGTGTGACTGAAGTCTTGAT	<u>4709</u>	GAGTGAAGTAAAGAAATCAAGAC	<u>4734</u>
B0696D03-A1 x		BACend		AGGAAGAACAGAAAGCAGTCTTT	<u>4710</u>	GTCATTATTTCTCTCAAAAGACTG	<u>4735</u>
B0700H07-A1 x		BACend		TCCTGGGAAGCAAGAAATAGGAA	<u>4711</u>	TGCGAGTGGCTTTTGTTCTATT	<u>4736</u>
B0726A20-A1 x		BACend		ACTGTTGTCACTCTGGGAAAG	<u>4712</u>	AGCTCTCCAGGTCCTCTTCCCA	<u>4737</u>
B0761L21-A1 x		BACend		GAGTAAAGAAATGTGTATAGGG	<u>4713</u>	TTTTTTGACCCACCCCTATAC	<u>4738</u>
B0814G06-A1 x		BACend		CGAGGAAGATGTAAGAGACTGT	<u>4739</u>	ATTGAGGCCCCAGAACAGTCTC	<u>4768</u>
B0857A05-A1 x		BACend		TCCTTAGTCTCTTTGGGAGAGCT	<u>4740</u>	ATTTTCCACAGGAAGCTCTCC	<u>4769</u>
B0895C23-A1 x		BACend		AGGTGCTAACCTCGCTCAATCTG	<u>4741</u>	GGGCTGGTTGCTCACAAGATTGA	<u>4770</u>
B0949E15-A1 x		BACend		CTTTTGAAGACGTGGGTTCTGT	<u>4742</u>	GAATGCAAGCAGCTCACAAGAAC	<u>4771</u>
B0604M16-A1 x		BACend		AGCCATTAACACACATTTCTAT	<u>4743</u>	GATGCTCTGTGCATATAGAAAT	<u>4772</u>

B0615D12-A1 x	BACend	TCCACTGAGAGTTACCAAAACC	<u>4744</u>	GGTATGAGAAITGTGGGTTTGG	<u>4773</u>
B0633K01-A1 x	BACend	GTTGACATTTTATCTGGGTAT	<u>4745</u>	ACTGATGACATTTTGATACCCAA	<u>4774</u>
B0663H23-A1 x	BACend	GAGGTCCCTATTGCTGTGTTTT	<u>4746</u>	CAGCCAAITGAAGTCAAAACACA	<u>4775</u>
B0696L08-A1 x	BACend	ATCTGTAGCCTATAGTGAACAG	<u>4747</u>	TTTACAGTGTTTGCCCTGTTTAC	<u>4776</u>
B0702C13-A1 x	BACend	GTAGTAACAGAAITGCATTTGA	<u>4748</u>	AGAGAGGAACAGCATCAAAAGTC	<u>4777</u>
B0702F18-A1 x	BACend	CTCTGCATTTCTTACTCTCTTAC	<u>4749</u>	AAGCTTTACTACCAAGTAAAGAG	<u>4778</u>
B0728K24-A1 x	BACend	TCGCAAAITAGCAACAAGGCATT	<u>4750</u>	CACCGTTATGCAGAAAGTCCCT	<u>4779</u>
B0738O20-A1 x	BACend	TGAAGTTGCGAAATCCCTGATAG	<u>4751</u>	AGGTTCCCTACTGAGCTATCAGG	<u>4780</u>
B0866B05-A1 x	BACend	AGCAGAAAGAGCAGACCCCTTCAA	<u>4752</u>	GGAGCATCCCAATCTTTGAAGGG	<u>4781</u>
B0598D10-A1 y	BACend	AGATGCTTATACTTGGTGTAAAG	<u>4753</u>	TACTTACACAGTTGGCTTACACC	<u>4782</u>
B0635H04-A1 y	BACend	AGTCACACCTTATGAGGCATCA	<u>4754</u>	CTGTATGAATCCTCTGATGCCCT	<u>4783</u>
B0666B20-A1 y	BACend	ATCCTGCTTTGTGGGTAGCCAC	<u>4755</u>	AATGCCACGGTGCAGTGGCTTAC	<u>4784</u>
B0700H07-A1 y	BACend	ACTCAAAACCAACCTTCCATTCA	<u>4756</u>	GGTTAGGATTAGTGTGAATGGA	<u>4785</u>
B0726A20-A1 y	BACend	TCAGTTCTCAGTCCTAGGAGAC	<u>4757</u>	GGTCTTCTACTCCAGTCTCCTA	<u>4786</u>
B0761L21-A1 y	BACend	GCGAGGGCTGCTGTCTTTCTCA	<u>4758</u>	AAATTAGCCAGGCATGAGAAAG	<u>4787</u>
B0814G06-A1 y	BACend	GCAGAGAGGTGGTGAGTGCAATC	<u>4759</u>	TGACAGTTTCTTTTGTATGCACCT	<u>4788</u>
B0857A05-A1 y	BACend	TGCTTATCAAGATGCCTTTGCC	<u>4760</u>	AATCAGGCCATGAGGGCCAAGG	<u>4789</u>
B0895C23-A1 y	BACend	CCATCCTTCATCCCGCAGCACTA	<u>4761</u>	CCCTGAATTTAGGTTTACTGCTG	<u>4790</u>
B0931G12-A1 y	BACend	AGAACCAGGCGACAGACTTACCCTGG	<u>4762</u>	CTGGACCAGGAATCCAGGTAG	<u>4791</u>
B0949E15-A1 y	BACend	ACTAGCTATTGAAGTGACTATC	<u>4763</u>	ATGGGCAAAAGAAATAGATAGTCA	<u>4792</u>
B0604M16-A1 y	BACend	GTTTCAGCTGTGGAATAIGTTA	<u>4764</u>	TGTCCTCCTCCCTTACATTT	<u>4793</u>
B0633K01-A1 y	BACend	ATGCTGCTTCATATTAACACATT	<u>4765</u>	CGGGAAGCATTTTGCATGTGTT	<u>4794</u>
B0663H23-A1 y	BACend	CTCGCTCCATCTGCGATGCACA	<u>4766</u>	AGGTGATCACAGACTGTGCATC	<u>4795</u>
B0696L08-A1 y	BACend	TGTTGTGTCAAGAACTCAGGAA	<u>4767</u>	ACCCAGCTGAATCCTTCCCTGAG	<u>4796</u>
B0702C13-A1 y	BACend	TCATGGGGGTGCTTTGACCCTTG	<u>4797</u>	TGGCCTCAAAAGGCTCAAGGTCA	<u>4826</u>
B0702F18-A1 y	BACend	CATGGTCACTGCAGCCTCTCA	<u>4798</u>	TGGCTAGAAAGAGGTGAGAGGC	<u>4827</u>
B0738O20-A1 y	BACend	AGAAAGCGGGGTGAGCAGGACAT	<u>4799</u>	GTTACCCCGGAGGATTAATGTCTG	<u>4828</u>
B0866B05-A1 y	BACend	GATGTTGTCCGACAGGCATGGG	<u>4800</u>	TTCTGTGTAGATCCCATGCC	<u>4829</u>
B0883G23-A1 y	BACend	GTTGGTAGAATTGGCAAGCCTTG	<u>4801</u>	CTCCAATCAGTTGCCAAGGCTT	<u>4830</u>
B0909L16-A1 y	BACend	GGTAAAGGACACTTCAAGGGAG	<u>4802</u>	TGGAGTGGCCCTGTTGTCCCTTG	<u>4831</u>
B0974M10-A1 x	BACend	ATGCAAAAGGCTCAGGAGCAAAA	<u>4803</u>	CCCTTCTGAGACAATTTGCTCC	<u>4832</u>
B1118L08-A1 x	BACend	GGCATGTAGATCAAAATGAATAA	<u>4804</u>	TGCTCCTTAGCTGAATATTTTCAT	<u>4833</u>
B0723P10-A1 x	BACend	GGTAGCAGTCTTACACTGCTGG	<u>4805</u>	CCTTTCCGATGACCCGAGCAGT	<u>4834</u>
B0748H09-A1 x	BACend	TGCCATGTAGCGTTCAATTTCC	<u>4806</u>	GTTTTCTGTGCAAGGGAATATG	<u>4835</u>

B0825F09-A1 x		BACend		ATACCCACAGGGTAGTACAGT	<u>4807</u>	TTGTGGCTCAATCAGTGTAC	<u>4836</u>
B0825K21-A1 x		BACend		CGTGAGGCCATTTCAACCACAC	<u>4808</u>	TCCCTGTCTTTGAAGTGTGTT	<u>4837</u>
B0845N16-A1 x		BACend		ACATATGAAAAAGACCGTAGAAA	<u>4809</u>	CAATTACAGGCACTTTTACG	<u>4838</u>
B0894N08-A1 x		BACend		ACGTGGAGAAAGCCGCTGTCTT	<u>4810</u>	CTGGACATTGAAATAAGACAGC	<u>4839</u>
B0956I1-A1 x		BACend		TGAATTTTAACAGGTGGCAAG	<u>4811</u>	ATTCCATCTGACAGCTTTGCCA	<u>4840</u>
B0974M10-A1 y		BACend		CTCATAGTTGTTACACACTCTG	<u>4812</u>	AAGCACGCTTTGAACAGAGTGT	<u>4841</u>
B0646E20-A1 y		BACend		CTCCATAGGAAGCAGCCATCAG	<u>4813</u>	ACTGGACCCAGCAACTGATGGC	<u>4842</u>
B0723P10-A1 y		BACend		TGTACCAACTGTTGACTATTA	<u>4814</u>	GTTTGCCCTCATGCTTAATAGTC	<u>4843</u>
B0748H09-A1 y		BACend		GCCTGGACAGGACACAATTGCA	<u>4815</u>	TTCCGGGTTTGATGTGCAATTG	<u>4844</u>
B0825K21-A1 y		BACend		CAATTAATTAGTTCCAAITGGCGC	<u>4816</u>	CACAGTCAGAGTTGGCGCCATT	<u>4845</u>
B0845N16-A1 y		BACend		GAGTGCCTACCGGAAAGAGAAGA	<u>4817</u>	TCCAGAGGCCAACTGCTTCTCT	<u>4846</u>
B0894N08-A1 y		BACend		TGCGTTTCTTCTTAGAGCTCC	<u>4818</u>	CACTCTGGATTAGCTGGAGCTCT	<u>4847</u>
B0956I1-A1 y		BACend		TGTGGGATGCTTCAGTTTTGT	<u>4819</u>	GATGAGTAGATCCCAAAAAC	<u>4848</u>
B0961F22-A1 x		BACend		CATCTGCGCTCGGGTCTGAAC	<u>4820</u>	GGTCACTGCAGGAAAGTTCAGA	<u>4849</u>
B0588P16-A1 x		BACend		AAGAAAGACCTCAACCCAAAGGC	<u>4821</u>	ACCCATGTGTGTCAAGCTCTTG	<u>4850</u>
B1000B21-A1 x		BACend		TATTACAGAGGCTGGTGATCAG	<u>4822</u>	TAGCCTGTGAGAAGCTGATCAC	<u>4851</u>
B0839D11-A1 x		BACend		GACAACCTTGCCTTCTTACCTG	<u>4823</u>	AGATGACCTATTGCCAGGTAA	<u>4852</u>
B1052D15-A1 x		BACend		CAGAAGCATAGAAACAATCCAG	<u>4824</u>	GCACCTGTTTATTAACCTGGATTG	<u>4853</u>
B1093F08-A1 x		BACend		TGCTGGCACTGCCAAAGAAATTC	<u>4825</u>	CCCTGGCGTTGCAGGAAATCTT	<u>4854</u>
B1134M23-A1 x		BACend		GAAITGGGGAGAAAGGGCAAGG	<u>4855</u>	GCTCGTTAAGAGTTCCCTTGCC	<u>4854</u>
B0894M06-A1 x		BACend		TCITTTCAITCTCTAATGGGCAC	<u>4856</u>	TGGGTACATGCACGTGCCCCAT	<u>4885</u>
B0895J20-A1 x		BACend		ACAGACACCTTGGGTCAITGACT	<u>4857</u>	GGAACCTGGAITGTAAAGTCAITGA	<u>4886</u>
B0961F22-A1 y		BACend		CAGTGGTCCCTCTCTCAITGAGT	<u>4858</u>	CTGCTTCTTAGAACAACTCATGA	<u>4887</u>
B0668P23-A1 y		BACend		ACATGATGCACCCCTTACCCTT	<u>4859</u>	CCGCTGTGTCTCCAGAACGGTAA	<u>4888</u>
B0588P16-A1 y		BACend		ACATGGGCTCAGACGAAAGATCT	<u>4860</u>	CACGACTTAGGAGGAGATCTTC	<u>4889</u>
B1000B21-A1 y		BACend		AAGAGAAGTCTGGAGACTGTGTC	<u>4861</u>	TAGCAAGTCTTATCGACACAGT	<u>4890</u>
B0839D11-A1 y		BACend		CCACTCAACCCACAATCTAGTCT	<u>4862</u>	GAAATACAGGGGATGGGACTAGAT	<u>4891</u>
B1052D15-A1 y		BACend		CCACCAAAATGGAATCTGTTGACT	<u>4863</u>	ATCAGAGGCTGTGTAAGTCAACA	<u>4892</u>
B1093F08-A1 y		BACend		AGGCGCGTTTCTTACTACAGAA	<u>4864</u>	TCGAAACAGCTGCCCTTCTGTAG	<u>4893</u>
B1134M23-A1 y		BACend		ACAGAAAGGCCGTGGGTAGAGA	<u>4865</u>	TTCTTCATTTACAGCTCTCTACC	<u>4894</u>
B0894M06-A1 y		BACend		CACATCGCTGCTTGACAGAACT	<u>4866</u>	GGGTCAITGTGACTGAGTTCTGT	<u>4895</u>
B0895J20-A1 y		BACend		CACATTTCTGAGACACTTGTCTA	<u>4867</u>	TAATACCTGGCAATGTAGCAAGT	<u>4896</u>
B0604N13-A1 x		BACend		ATGAGTCTCTCCACCGAATGTG	<u>4868</u>	GAACTCAGTCTCTGCACATTCTG	<u>4897</u>
B0714L01-A1 x		BACend		TCATCAGTTTCTAGGAGCTTTCA	<u>4869</u>	GTAAGTACTCTCTCTGAAGCT	<u>4898</u>

B0754A14-A1 x	BACend		GGATGCGACAGTCACCTTTCAT	<u>4870</u>	TGCAAGGCGATATGATGAAGAG	<u>4899</u>
B0894M06-A1 x	BACend		GATTAGTGTATGTAGAGACA	<u>4871</u>	TGGTGACGAGATTGTTGCTCT	<u>4900</u>
B1128L12-A1 x	BACend		TTGGTGTGAATCAAGCATCAGG	<u>4872</u>	TGAGCACAGGAGTTCCIGATGC	<u>4901</u>
B0643F18-A1 y	BACend		GTGGATTAAACCGAGGTGGAAT	<u>4873</u>	CCTTTCCAGTTTGAATTCACCC	<u>4902</u>
B0714L01-A1 y	BACend		GGCAATCTTTGCTGCTGCTTCTG	<u>4874</u>	GAATACTGCAGAGCAGGAAGCA	<u>4903</u>
B0754A14-A1 y	BACend		ATCCTGGGCAAGGAGTTTCAG	<u>4875</u>	CTGAGCCACACCTTCTGAAACT	<u>4904</u>
B0894M06-A1 y	BACend		TTGTTACATCGCTGCTTGACA	<u>4876</u>	ATGTGACTGAGTTCTGTCAAGC	<u>4905</u>
B1128L12-A1 y	BACend		GCCTTGAACCTGCACCTCAGCAGGA	<u>4877</u>	GTGCTTCTAACTTCTCTGCTG	<u>4906</u>
B0687F10-A1 x	BACend		TCCTCAAGCCACCTTCTATGT	<u>4878</u>	ACGTGAATCACGGAAACATAGAA	<u>4907</u>
B0791C09-A1 x	BACend		ACTGTGGCTGCACATAGGGATA	<u>4879</u>	AAAGCTTCTGGGGTATCCCTA	<u>4908</u>
B0820N16-A1 x	BACend		GGACCCACCCCTGTCAATTTTCAT	<u>4880</u>	GGGGCGATGGGAATATGAATT	<u>4909</u>
B0880M22-A1 x	BACend		TGTTTGATATGTTGGCTTACTA	<u>4881</u>	TGTGTCTTTTGAAGTTAGTACC	<u>4910</u>
B1008L21-A1 x	BACend		ATCTCTGGGAAGCTCTACAGTG	<u>4882</u>	CTCAATCCCTCCCACTGTAG	<u>4911</u>
B1043N20-A1 x	BACend		AGATAATGGGTTGCTTGGGCTC	<u>4883</u>	GTTAAAGCAGTTATGAGCCCAA	<u>4912</u>
B0700H07-A2 x	BACend		CTTGGACTCAAGACATCTCTCTG	<u>4913</u>	TGGGAGACTGAGACCGAGAGAT	<u>4942</u>
B0687F10-A1 y	BACend		TTTCAGTACTGCTCTTCCGTT	<u>4914</u>	TGGCTGTAGTGAATAACGGAG	<u>4943</u>
B0791C09-A1 y	BACend		CATTAGAAAGCCAGGAGGAAAC	<u>4915</u>	CTCCTTCTTCCGAGTTTCTC	<u>4944</u>
B0880M22-A1 y	BACend		CTATGTTGCATAGGAGTAGTGA	<u>4916</u>	AAGGATACCCTCTCTCACTACT	<u>4945</u>
B0909E24-A1 y	BACend		CCCTCTATAACATTTTCTCCCA	<u>4917</u>	CTTAGGACAAACCCCTGGGAGAA	<u>4946</u>
B1008L21-A1 y	BACend		GAGCCCTGCTCAGAAITTTTCATG	<u>4918</u>	GAGGCAAGGCTTTTCATGAAAT	<u>4947</u>
B0923H14-A1 y	BACend		GCAGCCTTACTGAGCTGACAGT	<u>4919</u>	CCGTCCATGGGAAACACTGTGAG	<u>4948</u>
B0979G13-A1 y	BACend		CTCCACCCTGATGGGTCACACTT	<u>4920</u>	ATTAAAGTTCTTGAAGTTGAC	<u>4949</u>
B1020H18-A1 y	BACend		CATGATCTCAATTAATTGCAACT	<u>4921</u>	GAAGAAAAACAGAGAGTTGCAA	<u>4950</u>
B0756E08-A1 y	BACend		ATGGGATCACTATGATAGCA	<u>4922</u>	TTTAAAAATTCACCTTGTATGC	<u>4951</u>
B0666F01-A1 y	BACend		GTGTCTCTGTGAACGGCTCTGA	<u>4923</u>	AATCAGAGTTTCTTCAGAGCC	<u>4952</u>
B0883G19-A1 y	BACend		ACATTTCCAGCTCTACATTCTA	<u>4924</u>	CTGAGTTTCTCCTACATGATGT	<u>4953</u>
B0923H14-A1 x	BACend		GATTAGAGAGGGTAGGAGGGT	<u>4925</u>	ACCTTCCAAACCATCACCTTCT	<u>4954</u>
B0781118-A1 x	BACend		GGATTAAATAGTACCACCCCTTG	<u>4926</u>	ATTTAACACAAAGGCAAGGGGT	<u>4955</u>
B0979G13-A1 x	BACend		GACATTTCATGCAATGCAACAC	<u>4927</u>	CCCGCTTGCTTTTGTGTCCAT	<u>4956</u>
B1020H18-A1 x	BACend		CATATGGCTAAGGCTCTATCTA	<u>4928</u>	AATCAGCAGGTACATAGATAGA	<u>4957</u>
B1029H23-A1 x	BACend		CAGCTAAGGGGAGAGTGCAGAG	<u>4929</u>	CGAAATGCCGACTGCCGTGCAC	<u>4958</u>
B1076C21-A1 x	BACend		CTAGAAATTTCCATGTAGTAAGA	<u>4930</u>	ATACTTGTCTTCTCTTACTA	<u>4959</u>
B1104N09-A1 x	BACend		CCTGCTGATGAGCAAAAGAAIA	<u>4931</u>	CACCTGGGTACTTCTTATTCTTT	<u>4960</u>
B0663J16-A1 x	BACend		CAACCACTATCTGCTGCCCTTC	<u>4932</u>	TAGGTGAGTCTCTTGAAAGCAG	<u>4961</u>

B0656F13-A1 x	BACend		GGTGTGGAGAGAGTGGACTTAA	<u>4933</u>	TAATATAAATCTTAGAGTCC	<u>4962</u>
B0883G19-A1 x	BACend		CATGGCAGAGGTGATAGAGTGA	<u>4934</u>	ATAATCCAGGAGATCACTCTA	<u>4963</u>
B0760A04-A2 x	BACend		GCCTCATGATTTGGGCATGCT	<u>4935</u>	GTTCAAAATCTGCCAAGCATGCC	<u>4964</u>
B0785D22-A1 x	BACend		GTAACACAGGCTAACACTGTTAA	<u>4936</u>	ATGCGTGTGCTGTTTAAACAGT	<u>4965</u>
B0723P10-A1 y	BACend		TGGAAGCCACTTAGAGGTTGCA	<u>4937</u>	AACAGTTTGGTACATGCAACCT	<u>4966</u>
B1095L07-A1 x	BACend		TCTAAAGATGGGGCCTACAGT	<u>4938</u>	ATGGCTTCAGTTTACTGTGAG	<u>4967</u>
B0997104-A1 x	BACend		TACTTTACTCTGTTTCTCTGTA	<u>4939</u>	AAGTGATATGAGACATACAGGA	<u>4968</u>
B0723P10-A1 x	BACend		AGGAAGGGGAAATAGAAAGGGA	<u>4940</u>	TAICTGCGTGGTGGTTCCCTTC	<u>4969</u>
B0997104-A1 y	BACend		AGTGTAGTGGGAATGAGGAGT	<u>4941</u>	CTCCATTATCAGTCACCTCTCA	<u>4970</u>
B0880L16-A2 x	BACend		GAATCCCATCATCAGCACAAGG	<u>4971</u>	TTTGTGCTGGCTGGCCTTTGTG	<u>5000</u>
B0598021-A2 x	BACend		CGCCGAATTCATGACTCTTGA	<u>4972</u>	TTTGGCAGAAATGTTTCAAGAGT	<u>5001</u>
B0768112-A2 x	BACend		CACAAAGACAGACCCACAGCTC	<u>4973</u>	GCTGTGGGAAATGTGAGCTGTG	<u>5002</u>
B1056C02-A2 x	BACend		CCACACAGGAAACTGCCATCT	<u>4974</u>	CCAATTTCTCCTTTTCAGATGGCA	<u>5003</u>
B1056C02-A2 y	BACend		GAGACGTGAGTCAGGACAGGTG	<u>4975</u>	TGCCCAATCTGTACCACCTGTG	<u>5004</u>
sis-AA017225	BACend		GATGCCAGGAAGTACTGGTAA	<u>4976</u>	GCAATCTCCAATCTTACCAGG	<u>5005</u>
A004F14	EST		GGAACCCCGTGACTTGACTTAG	<u>4977</u>	TGTCAATGAGCACCCTTAAGTCA	<u>5006</u>
SGC31333	EST		AGGTGGTGAATCTAGTCTCCGCT	<u>4978</u>	GAGTGAAGGTGGAACCGGAGA	<u>5007</u>
WI-12422	EST		AACAGACAGCATCTCTGGAGAGA	<u>4979</u>	CACAGAGAGTGCAATTTCTCTCA	<u>5008</u>
sisG21539	EST		ATGCATACAGCAGGCCATTGTG	<u>4980</u>	CAGCCCTATGACCACAATGG	<u>5009</u>
WI-13120	EST		GGGAGCTACAGGTGATAGCTAT	<u>4981</u>	GGGCGCATAGCTATCACTGTGA	<u>5010</u>
sisG22703	EST		CACAGAGACACAGAGACTCGAA	<u>4982</u>	AACATGGACAGGCCCTTCGAGTC	<u>5011</u>
sisG36097	EST		TGAGCAGTCTGACCTGCTCTC	<u>4983</u>	AGCTGGAGCACCTGGAGAAAGCA	<u>5012</u>
sisG9807	EST		CAGCCAGCTACTGAACCTTATG	<u>4984</u>	TGGCCCTAGGCACACATAAAGT	<u>5013</u>
sisG15434	EST		TACCACCACTCTGCCAGATGG	<u>4985</u>	GTANTCTGTGGCCGCCACTCTGC	<u>5014</u>
sisG30525	EST		GGCACACAGTCTGCAATGCTTG	<u>4986</u>	TAGGGACATCCCTCAAGCATT	<u>5015</u>
A007A34	EST		TGTTCTGGCAGATTCCATCATC	<u>4987</u>	CTTATGTTGGATTGATGATGG	<u>5016</u>
A006D44	EST		CAGGGTCATTTGAGGAGGAACA	<u>4988</u>	CGAAAGCTTGAATCTGTTCTC	<u>5017</u>
SGC30248	EST		GATCGAAGCAGCACAGAGCAGT	<u>4989</u>	CTCCTTCCACAGACACTGCTCT	<u>5018</u>
sis-N20163	EST		TCTCTACCAAGCAATACTTCAC	<u>4990</u>	CTGAATTCAGTGTAGTGAAGTA	<u>5019</u>
Cd80a01	EST		AAAGGCCACACAGCCCAATC	<u>4991</u>	GGCCTGCAAGTGATGATTGTGG	<u>5020</u>
Cd80ca07	EST		AAGCTGACTTCAATCGGTAC	<u>4992</u>	TGCTAAAGCCTCATGTACCGAT	<u>5021</u>
sisG3292	EST		AAGCTGACTTCAATCGGTAC	<u>4993</u>	TGCTAAAGCCTCATGTACCGAT	<u>5022</u>
SGC34088	EST		AAGTCAATTGCTCCCATCTGC	<u>4994</u>	CTTGTTGTTGCTGGCAGATGG	<u>5023</u>
WI-12272	EST		GACTCATATGACAGACCTTGAA	<u>4995</u>	TGTCCACCTTTCTTCAAGGT	<u>5024</u>

SISG16387		EST		CATGATCCTCCAGACCCCTTAGA	<u>4996</u>	TGCCCAATTCCTGCTAAGGG	<u>5025</u>
SGC31722		EST		CAAACGGAGAAAGCCCGAGATAC	<u>4997</u>	TTGTTACTGTACGTGTAATCTGG	<u>5026</u>
WI-15018		EST		AGTGACAAATTAGAGCTCTGGGG	<u>4998</u>	GGTCTTCATTCTCCCCAGAG	<u>5027</u>
WI-18492		EST		TGCTTGGCCAAACAGACTTTCCT	<u>4999</u>	TGATGAGACTGCAGAGGAAGTC	<u>5028</u>
SISG9546		EST		ACCTGAGAGCAGGGAGATTCCA	<u>5029</u>	TAACTCTAGCAGCTGGAATCT	<u>5058</u>
A006016		EST		CCCGAGGGCTTCTCTGAACACTA	<u>5030</u>	CTCACAGCGCTTCTAGTGTTC	<u>5059</u>
H64839		EST		AATCTGAGGCACACAGAGAGT	<u>5031</u>	ACTGAGCTCCTTTCACCTCCT	<u>5060</u>
SISG3357		EST		GCCTTGCTAACTGTACCAATAGT	<u>5032</u>	CACCTGCAGGAATTAATATGTT	<u>5061</u>
SISG30906		EST		TCTAAGGTTCCGGATGACGTG	<u>5033</u>	TGTCGCCCAATTCACGTCGA	<u>5062</u>
SISG26056		EST		GAGTTACAGGAAGTGGTTCCCG	<u>5034</u>	CTGGGTGTGTGTACAGGGGAACC	<u>5063</u>
SGC30786		EST		ACAGCTCTCCTTCTTAATGCC	<u>5035</u>	CACCCCTATCTCTGGGCATTAA	<u>5064</u>
SIS-N59820		EST		AGACTGCATCTTCGAACAACAGG	<u>5036</u>	ACTGGGAATCTAGCGCCTGTTGT	<u>5065</u>
SISG42115		EST		TTCTCGAGGGTTCTCTGCTTCACT	<u>5037</u>	AGTTCTCTCGGGAGTTAGTGAAGC	<u>5066</u>
FB9F8		EST		GAAAAACCCCGCACCTTGACACAMC	<u>5038</u>	CGTCCAGAAAAGTAAGTTGTGTG	<u>5067</u>
AA252357		EST		CAGCCATCGAGTCTCTCAATCCG	<u>5039</u>	CCAGACTTTCCTCACTCGGATTTG	<u>5068</u>
SISG4720		EST		TCGAGAAAGGCTGTTCCTACAGAG	<u>5040</u>	TAACTCAGGACCTTCCCTTTGAG	<u>5069</u>
SIS-AA001424		EST		AAGCTGCTCTTCTCAGCTACTCTG	<u>5041</u>	TTTCAGGGTTCTGGGTACAGTAG	<u>5070</u>
SISG31443		EST		CAAAGCAGCTGAGCTGAGAGAATTC	<u>5042</u>	GGTGATACAGTGTGTGAATTTCTC	<u>5071</u>
WI-6385	D12S1405	EST		TAAAGGCAAAAGGCCACACAGCCCA	<u>5043</u>	CTGCAGTGATGATTGTGGGCTGT	<u>5072</u>
A008705		EST		TAAAGATAAGGGCTGGGCTTTGAC	<u>5044</u>	AACCTCGGACACTGTCAAGC	<u>5073</u>
RS0113		EST		TCATACCAAGTGCTGGCTGCTAAG	<u>5045</u>	CCAGTTTCTGCACATCTTAGCAG	<u>5074</u>
SIS-H94865		EST		CTCTAAGAACCAAGACCCCTCAGTTG	<u>5046</u>	CTCATTCCTTACTGGCAACTGAG	<u>5075</u>
A006R19		EST		GGTTTGAACAGTGGGAGATACCAAG	<u>5047</u>	TTTTCTCCTCCCACTCTGTATC	<u>5076</u>
SGC34278		EST		CAAACACAAGAGTCTCTTGTCTG	<u>5048</u>	ACAGTCAATGGAAGGCGAGCAAGA	<u>5077</u>
A004B47		EST		GTCGCCCTGTGAATTTGGCCTTTCT	<u>5049</u>	GCTGGAAGCAGAAAGAAAGAAAGGC	<u>5078</u>
SISG40199		EST		GGAAGGCTGTCTTCTTTCTTACCAC	<u>5050</u>	TGACACCTGCTCATGTGTAGTA	<u>5079</u>
SISG8935		EST		CAAACACAAGAGGTCTCTTTGCTG	<u>5051</u>	ACAGTCCATGGAAAGGCAGCAAGA	<u>5080</u>
SISG4731		EST		GCAATGTTGTTTCTGTCTGGGAT	<u>5052</u>	AGCAGACAAGATCTAGATCCAGA	<u>5081</u>
SISG8142		EST		GTCGCCCTGTGAATTTGGCCTTTCT	<u>5053</u>	GCTGGAAGCAGAAAGAAAGAAAGGC	<u>5082</u>
A005X42		EST		GCAATGTTGTTTCTGTCTGGGAT	<u>5054</u>	AGCAGACAAGATCTAGATCCAGA	<u>5083</u>
CDA18G06	D12S1205E	EST		ACAGACTACAAAGCTCAATGAAGCC	<u>5055</u>	TCCGACCAATGCCAGGAGGCTTCAT	<u>5084</u>
STSG40222		EST		TCTTCTCTCTCACTGAGACCATG	<u>5056</u>	TGCCACATGGAGAAACATGTCT	<u>5085</u>
SIS-R5615		EST		GCTAGTGAAAGGATACCTGAAG	<u>5057</u>	CTTCTGTGGTAGTGTCTTTTACAG	<u>5086</u>
SIS-R02295		EST		CTCAATCCAGATGACAAGCCTTTG	<u>5087</u>	ACCTAGTATCCTACTCAAAAGCGT	<u>5114</u>

sis-R81342	EST		GGCAAAAGGAAAAACCATGATG	<u>5088</u>	TCACCTCCCTTACAGTCATACATG	<u>5115</u>
sis-H65839	EST		AAATAGATTGATTGCCGTCCTCAAC	<u>5089</u>	AAATATGTGCTAACTGTTGAGGA	<u>5116</u>
sisG52716	EST		AGATGGGGGAGACAAACGGTTAAAC	<u>5090</u>	CGGAAAAGAAACATCTGTTTACCG	<u>5117</u>
sisG54813	EST	highly similar to 22 kd peroxisomal membrane protein	TTTGTTGGTGCAGCTGGTCCAAACA	<u>5091</u>	TGCAGTAATGGATGGGTGTTGGA	<u>5118</u>
sisG50504	EST		CCGTAATACCCAGACTACACACTG	<u>5092</u>	CACCAATGGCAATAGCACAGTGTGT	<u>5119</u>
sisG48386	EST		CCAGCAGCAGGATATTGTGTACGT	<u>5093</u>	GTTTACAGCCTACAGGACGTACAC	<u>5120</u>
sisG54842	EST		TTCTTTCTTCAGGTCGCCGCTCAAG	<u>5094</u>	TCACGGCCTACGAGATCTTTGAGC	<u>5121</u>
sisG53600	EST	Highly similar to peptide transporter PTR2	AACTGGGATGCCAACTAACACGTG	<u>5095</u>	AAGTCTTTGGGAACTCCACGTGTT	<u>5122</u>
sisG53541	EST	Homo sapiens hwi	AACCCACCTATGTTGTAGTGAG	<u>5096</u>	GGCGTAAAGTAGGATGCTCACTAC	<u>5123</u>
sisG53307	EST	miRNA, partial cds	GAGGCTAGGCTGAATATAAACCAAG	<u>5097</u>	CACTGCCAGTCAGCAACCTGGTTA	<u>5124</u>
sisG63473	EST		CCACTGGCTGCATTTTCCAGCTTT	<u>5098</u>	CACCAAGTACTAGAGAAAAAGCTGG	<u>5125</u>
sisG54325	EST		CGGCACAAGCAGATTTCAGATCAG	<u>5099</u>	CTGGGGGAAATGCTGACTGATCTG	<u>5126</u>
sisG52343	EST		AACGTGAGTCAAGGTGATCACGAAAG	<u>5100</u>	CCAGTGAATAAGCCCCCTTCGTGA	<u>5127</u>
WMAF-856	EST		AAGTCAATTGCTCCCATCTGCCA	<u>5101</u>	TCTACTTGTTCGTTGCTGGCAGAT	<u>5128</u>
sisG47723	EST		CTGAGTTCTCTTAGCAGCTTCGTA	<u>5102</u>	TCTTCAAAAGACCTCCTACGGAAG	<u>5129</u>
sisG60065	EST		GGAGGTGAATAAGCTGATCTCTGA	<u>5103</u>	GCTGGGTAAGTAAAGTGCAGGAT	<u>5130</u>
sisG46424	EST		GGACACATCTGTTCATCTTCACC	<u>5104</u>	CCCATGAGTTGTAGTGGTGAAGA	<u>5131</u>
sis-U79526	Gene	DEZ	TGATCCTCACTGTGGAACCCCT	<u>5105</u>	GAGAGAGTCCATTGAGGGGTTG	<u>5132</u>
SGC31491	Gene	NOST	AGAGCGGCTCTTTTAATGAGGG	<u>5106</u>	GGGAGACGTCGCAACCCCTCATTT	<u>5133</u>
sisG1936	Gene	CLA-1	TCAGTCCATAGGATGATGTAG	<u>5107</u>	TCCTCCAGCCCTAACTGACATC	<u>5134</u>
sis-W31616	Gene	UBA52	CCAGCAAGATCAACCTCTGTC	<u>5108</u>	ATCCCTCCTGATCAGCAGAGGT	<u>5135</u>
ZNF10	Gene	KOX 1	ATGTGGGAAGGCCTTGGTAGT	<u>5109</u>	GTAAGGTTTGAGCCACTACCAA	<u>5136</u>
ZNF26	Gene	KOX20	GTGAATGTGAAAAAGCCTTCAC	<u>5110</u>	GAGATGACTTCTGAGTGAAGGC	<u>5137</u>
WI-6921	Gene	RNP24	GTTGCAAGTGTTCACCCCAAG	<u>5111</u>	AAACCATACCTCCACCTTGGGTG	<u>5138</u>
sis-D60472	Gene	SMRT	GAACGACGTGTGTAATGACAG	<u>5112</u>	AGGGTGGTGTATTCTGTCAATT	<u>5139</u>
WI-16177	Gene	RAN	CCTTCAGGCATCCACAGATGA	<u>5113</u>	CGGAACATGTGCTTTCATCTGT	<u>5140</u>
sisG1702	Gene	CAGH32	TCAGGCACCAATCTGAACAAGGG	<u>5141</u>	GAAAGTTGGATCCAAAGCCCTTGTT	<u>5170</u>
IB2452	Gene	ULK1	GCCATCAAGGTGATGAGGAAAGAG	<u>5142</u>	AAGAAAAATCCCCGCTGACTTCTCC	<u>5171</u>
sisG39493	Gene	CAGH32	GTGCTGAATCTCTTGCGTGACATG	<u>5143</u>	TAGTGAACCTTGGGACCAATGTAC	<u>5172</u>
A002A44	Gene	CAGH32	TGGTTCTCTGCTTCACTGGCAAA	<u>5144</u>	GGATTAAGCTTGTGTGTTCTGCCA	<u>5173</u>
sisG27206	Gene	GCP170	GAGCACATCTGGCCTGGCCAGT	<u>5145</u>	TGAGGTTCTGAGTCACGTGCCA	<u>5174</u>
CDA1JF08	Gene	GCP170	AGTGAAGCTCAGAAACACCTTCACACC	<u>5146</u>	AGTTGAGTGACGCTGTGGTGTGAG	<u>5175</u>

R39599		Gene	GCP170	ACTTCGTGACGTGATCGAGAACTCC	5147	CCCAACAAAAGATCCAGGACTTCT	5176
SlSG31494		Gene	ZNFI40	TCTCCAGTATGAGTCTCTGGTGT	5148	GCCTTTTCCCTGGTGTACACACAGA	5177
TH_a		Gene	MUC8	ATCCACCGCTAGAAACCCACTC	5149	GACCATCAACTGATGAGTGGGT	5178
SGC31491_a		Gene	NOS1	CCTAGTAGCTTTCTCCCAAG	5150	ATTGGAAAAGAAAGCCTTTGGGA	5179
SlS-X89576		Gene	MMP17	AGAGGAGCTGTCTAAGGCCATC	5151	TGCTGCATGGCTGTGATGGCCT	5180
SlSG43910		Gene	SFRS8	caglaacagttatccacacagac	5152	tgccataagtcgacagacac	5181
Pe99K7.T7	D12S2479	Genomic		AGAAAGCCCTCTCTCCCTCTCTC	5153	GTCAACATTTTGGGGTGAGAGAGG	5182
P493P14/T7	D12S2451	Genomic		TCTCAGGAACCAAGATCCATAG	5154	CAGTTAGATMAAAGCTATGAG	5183
P313C9/SP6	D12S2447	Genomic		CAGCTGAGGAAGTTACACAGGC	5155	AGGACCCAGTTGAAGCCTGGTG	5184
WI-5824	D12S2002	Genomic		CATTACCTGCCCGCCTGGTCA	5156	CAGGATTTGTGTGTGACCCAGG	5185
WI-10803	D12S1944	Genomic		CTGGATTTCCAGAGACTGACCT	5157	TCAGGCAATAGAGAAAGTCACT	5186
WI-2002	D12S1084	Genomic		ACAACAGAAGTTGTCACTGAAG	5158	CTGTTCAACAGTGCCTTCACTG	5187
WI-3045	D12S1420	Genomic		CTTAAGCGAGCAACCTGATAACCC	5159	TCCTAATCTGGCAGGTGGGTATC	5188
WI-3549	D12S1998	Genomic		GAGAACTCAGCTGCCATGTGTGAG	5160	GGACTCTTTGAGCACTCCTCACAAC	5189
WI-6077	D12S1322	Genomic		AGCAGCACTAGGCATGGCTGTT	5161	ATAAGAGCTGAGATAACAGCCA	5190
SHGC-12243	D12S1845	Genomic		CAAGCTTCCCTCTCTTCCCATTTGT	5162	TTCCGGCGTTGTAGTTACATGGG	5191
SHGC-13782	D12S1851	Genomic		AGTCAGGTACAGAGGTTCTGACAAC	5163	CACCTTGTTCGTCTCTGTGTGAG	5192
SHGC-14238_a	D12S1853	Genomic		CAAGTGTCCACATTTTCTCTGCA	5164	CCGCTCACTCACTCTGCAGGAA	5193
WI-3549_a	D12S1998	Genomic		CCATGTTGTGAGGATGCTCAAA	5165	ACCTTTTAGGACTCTTTGAGCA	5194
AFMB337xc1	D12S1675	MSAT		GATCTGCAGCATTTGAGGGAGCA	5166	GTCCTAGGCACATTTGCTCCT	5195
AFMa197z99	D12S1609	MSAT		GGGGATTTAGTAGNTCAATGTA	5167	GTCACTGGGTGACATACATTGA	5196
AFMB350Zb5	D12S1679	MSAT		GTTGTAGGCTTCTTGCCCTCTG	5168	CCCTCTACCATTCACAGAGGCA	5197
UT7009	D12S834	MSAT		GTCCAAGAGTGGGGAGTTGACC	5169	ATTGGATAGGCATAGGTCAACT	5198
AFMB301we5	D12S1659	MSAT		TCTAAGCTTTCGTTTGCCTGCT	5199	CACGTGCTTTTCAGAAAGCAGGC	5214
AFMa064x99	D12S1714	MSAT		GTTGAGATCCACAGGTGTCTA	5200	TGTAGCATATGATGTAGACACC	5215
CHLC A1A19A06	D12S2069	MSAT		TGTTGCCCTAGGCTGGTCTTGAA	5201	CTTGAGTCCCAAGAGTTCAAGAC	5216
ATA29A06	D12S1045	MSAT		GACCAGCCTAGGCACATAGTGA	5202	TTAGAGATGGGGTCTCACATG	5217
AFM210Zd6	D12S97	MSAT		AATTGTCATCATGGGGCTCGAA	5203	CCTTCACTGAGGAGTTGCAGCC	5218
AFM295ye9	D12S343	MSAT		TACTGCCACTCTCCAGAAATATC	5204	GATCTGGAAGGCTCGGATATTCT	5219
509/510	D12S63	MSAT		GTGGTTGGGTTAACAAAGAATG	5205	GAGAAAGCTGCAACGCATTCTTT	5220
AFMa275xb9	D12S1628	MSAT		AAGGTAGAGCTTGGCAACAGGA	5206	AGCCCCGCTGGACCTCTGTTG	5221
AFMB002v65	D12S1638	MSAT		TGCCAGAGGTTTAAGTTGGTT	5207	GAATGGCAATTTGGTAACCAACT	5222
GATA13D05	D12S392	MSAT		GTATGATAGCAGACGATAGAG	5208	TCTATCTGTCAATCCCTCTATCG	5223
12QTEL82	D12S2342	MSAT		TACATTTCCACCAAGCAGTGCACAAG	5209	TGGAGAAATTTGGAAGCCTTGTGCA	5224

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12QTEL87	D12S2343	MSAT		TTGTTAGGCTTCTGGGTTGGGTAC	<u>5210</u>	ACAGGCATTAGCCCCCTGTACCCAA	<u>5225</u>
AFMa082ze9_a	D12S1723	MSAT		CTTCGGTCATGAATGTCAGTAG	<u>5211</u>	TCTGCAGTGGTTCCCTACTGAC	<u>5226</u>
AFM156xc5_a	D12S1599	MSAT		TGGGAAGAGTTGCCCTCAGGAA	<u>5212</u>	CCCTTCTCAGTCCTTTCCTGGA	<u>5227</u>
AFMa123xe1	D12S367	MSAT		CTGTATTAAATGAGTCTGGGTT	<u>5213</u>	GGGTTAATACAGTTAACCCAGA	<u>5228</u>

Please replace lines 7-8 at page 144 with the following rewritten lines:

-- SEQ ID NO: 5229) and pBAC 3'-1 (CGA CAT TTA GGT GAC ACT; SEQ ID NO: 5230). --

Please replace lines 30-31 at page 145 with the following rewritten lines:

-- adapters (5' GTCTTCACACGGGG (SEQ ID NO: 5231) and 5' GTGGTGAAGAC (SEQ ID NO: 5232) in 100-1000 fold molar excess. These --

Please replace Table 5 on page 162 with the following table:

PLEASE SEE NEXT PAGE FOR TABLE

TABLE 5: PAIRED LINKERS

<u>Paired linkers</u>	<u>Sequence</u>	<u>SEQ ID NO:</u>	<u>Cell/Tissue Type</u>
OLIGO 3	5'CTC GAG AAT TCT GGA TCC TC3'	<u>5233</u>	Th2/unstimulated (dT+rp)
OLIGO 4	5'TTG AGG ATC CAG AAT TCT CGA G3'	<u>5234</u>	Th0/stimulated/anti CD3 (dT+rp)
			Pulmonary artery endothelium cells (dT+rp)
			Lung microvascular
			Endothelial cells (dT+rp)
			Bronchial epithelium cells (dT+rp)
OLIGO 5	5'TGT ATG CGA ATT CGC TGC GCG3'	<u>5235</u>	Normal Lung (dT+rp)
OLIGO 6	5'TTC GCG CAG CGA ATT CGC ATA CA3'	<u>5236</u>	Athmatic lung (dT+rp)
			Th2/stimulated/TPA (dT+rp)
			Bronchial smooth muscle cells (dT+rp)
OLIGO 9	5'CCT ACG GAA TTC TCA CTC AGC3'	<u>5237</u>	Brain (dT+rp)
OLIGO 10	5'TTG CTG AGT GAG AAT TCC GTA GG3'	<u>5238</u>	Th0/unstimulated (dT+rp)
			Pulmonary artery smooth muscle cells (dT+rp)
OLIGO 11	5'GAA TCC GAA TTC CTG GTC AGC3'	<u>5239</u>	Lung fibroblasts (dT+rp)
OLIGO 12	5'TTG CTG ACC AGG AAT TCG GAT TC3'	<u>5240</u>	Th0/stimulated/ TPA (dT+rp)
			Small airway epithelium cells (dT+rp)

Please replace Table 7 on page 165 with the following table:

TABLE 7: MODIFIED OLIGONUCLEOTIDES

Modified	SEQ	
Oligonucleotides	ID NO	Sequence
OLIGO 3	<u>5241</u>	5' CUA CUA CUA CUA CTC GAG AAT TCT GGA TCC TC 3'
OLIGO 5	<u>5242</u>	5' CUA CUA CUACUATGT ATG CGA ATT CGC TGC GCG 3'
OLIGO 9	<u>5243</u>	5' CUA CUA CUA CUA CCT ACG GAA TTC TCA CTC AGC 3'
OLIGO 11	<u>5244</u>	5' CUA CUA CUA CUA GAA TCC GAA TTC CTG GTC AGC 3'

Please replace Table 8 on pages 170-176 with the following table:

PLEASE SEE NEXT PAGE FOR TABLE

TABLE 8: SSCP PRIMERS

Primers used in SSCP experiments						
		SEQ			SEQ	
Gene	Exon	SSCP Assay	ID NO.	Forward Sequence	ID NO.	Reverse Sequence
454	A	55_454_A_F_56_454_A_R	5245	TGGCCCTGTACGGAAGATA	5271	CTGCAGAGATCTGGGTCCTC
454	B	57_454_B_F_58_454_B_R	5246	TTGATGCTTCCCATGCTG	5272	GGAGAATGCTACGAGGTGCT
454	C	59_454_C_F_60_454_C_R	5247	TCAAGGCCCTTGCAATTTCT	5273	GTCGCAATTTCTGCTTCTTC
454	D	61_454_D_F_62_454_D_R	5248	TCGCCACTCTGTCATCCTTC	5274	GAGGCTGAAGACCTGACCTG
454	E	63_454_E_F_64_454_E_R	5249	CCTCTCCGCAGTTCCTTTCAC	5275	GAGGGCCACTGTGTCTGTCT
454	F	65_454_F_F_66_454_F_R	5250	GTATCCCAAGACCAAGCCA	5276	AACTAAGACAGCCAGGCAGC
454	G	67_454_G_F_68_454_G_R	5251	ATGGAACCTCTCCACCACAC	5277	TCCAGTGTACAAAGCACCA
454	H	69_454_H_F_70_454_H_R	5252	CTGGCTATGCAGGGAGATGT	5278	GTGAGTTTGACCTGGGCT
454	K	71_454_K_F_72_454_K_R	5253	CCAGAACCCAGCACCTTCA	5279	AGGCTGAGACCAAAACCTT
454	L	73_454_L_F_74_454_L_R	5254	AACCAACAATTGCACGTTGA	5280	TGTGATGAGGAAGTCGATG
454	M	75_454_M_F_76_454_M_R	5255	CAGCGCTGTCTGCATTCT	5281	GGAATCTCTCCGTGCTTGG
454	N	77_454_N_F_78_454_N_R	5256	TGATAATTCTGTACAAAATGGTAA	5282	CTTTGTTAAATCCATCAGTTTTG
454	O1	79_454_O_F_80_454_O_R	5257	CCTAGAACCCTGAGGGCTTGTC	5283	CTGTGGCTCTCAGGGAGTTG
454	O2	81_454_O_F_82_454_O_R	5258	GGTGCCAGTGTGGAAGATG	5284	AGGTGGCGTAGCACCTGTAG
454	O3	83_454_O_F_84_454_O_R	5259	CACCACCTCAGAGCTGTTCA	5285	ACTGCCCTTCACTCTTTGGA
454	O4	85_454_O_F_86_454_O_R	5260	CCAGGACATGGCTGACTTTTG	5286	ACAGACAGGATTTGCGCTTG
454	AA	1959_454_AA_F_1960_454_AA_R	5261	GAAATAATTCCAATTTTGCTGG	5287	CCGAGGAAAGTGGAGTTGAG
454	AA	1961_454_AA_F_1962_454_AA_R	5262	CCTGTTTTGCCTTTGAGTCCA	5288	TACTCTCCACCCTCCTCTGC
454	AA	1963_454_AA_F_1964_454_AA_R	5263	CCTGTGATCTTTGGCTGAT	5289	ACAACCCCTTTATTACAGCCC
454	AA	1965_454_AA_F_1966_454_AA_R	5264	GGGAGATCTTCAATTTACC	5290	GTGTTTCAGAGGATGGGCATT
454	AA	1967_454_AA_F_1968_454_AA_R	5265	GGGAAAAAGGAGGAATTTCTAAA	5291	CCCTCCAGTAAGTGCMAAA
454	AA	1969_454_AA_F_1970_454_AA_R	5266	GCAGTCATTTGAGAGCCTTG	5292	GGAAAAGATGATCACGTGGAA
757	A	1750_757_A_F_1751_757_A_R	5267	GAGCAGGGGTGAGAGCC	5293	CAGGTTGGGCATACGAGTCA
757	A	1752_757_A_F_1753_757_A_R	5268	GCAAGGACATCGGCTACAA	5294	ATAATCGGGGAGCAGCTTGAG
757	A	1778_757_A_F_1779_757_A_R	5269	TGCACCGAGCAGGCTCTAC	5295	GTCTCTCAGCGGGTGTCTC
757	A	1780_757_A_F_1781_757_A_R	5270	AACTACCTGTGCATGAGGC	5296	GAAAGTGAGCACGGTGAAG
757	A	1758_757_A_F_1759_757_A_R	5297	CGTGCTACCTTCTCTCATC	5330	GTGAGGACCACCACACAC
757	A	1760_757_A_F_1761_757_A_R	5298	CTGTGTTGGTGGTCTCTC	5331	GTAGCAGGCCACGGGGAAT
757	A	1782_757_A_F_1783_757_A_R	5299	TCTGCTACGTGGGAGCAT	5332	CCATGTTGAGGCGTTGTA
757	A	1784_757_A_F_1785_757_A_R	5300	CTCTGTGCTGTACACCGTGC	5333	GGTTTTCTCCGGCTCTTCTT

757	A	1786_757_A_F_1787_757_A_R	5301	CCTCCAAGACTCTGCAGTCC	5334	CACAACCAAGAAAGCACCA
757	A	1788_757_A_F_1789_757_A_R	5302	AAATATGAGATCCCTGCCCA	5335	CTTCGCTGGAACCAACCAAC
757	A	1768_757_A_F_1769_757_A_R	5303	TGAAATTCAGGATGCTGTGA	5336	TTGCAAGCAGTTATCTGTCC
757	A	1770_757_A_F_1771_757_A_R	5304	TTGAGTTGGCTTTGCTACCC	5337	TGTGAGGTTTGTATGGAGGTTT
757	A	1772_757_A_F_1773_757_A_R	5305	CTGCAAGACAGAAACCTCCA	5338	TCCACAATCAGTCCAAACG
757	A	1774_757_A_F_1775_757_A_R	5306	TAATGGAACCAAGCCAATG	5339	CAATATACACACGCAGAAACC
757	A	1776_757_A_F_1777_757_A_R	5307	TGCCAGGAAGAGTGGTTTC	5340	GCTAGGAAGCAACCCACAGA
561	A	1530_561_A_F_1531_561_A_R	5308	AGGGATAGGATGCACGCC	5341	CTCCACCACACCAGGGAT
561	B	937_561_B_F_938_561_B_R	5309	ACACACATTTCCACCACCAA	5342	CATGAACGTGTGGAAAGGCT
561	B	939_561_B_F_940_561_B_R	5310	CCGAGCTCAAGTGAGCAGT	5343	ATTTCACCTGTGCACACCTT
561	C	941_561_C_F_942_561_C_R	5311	CATGACCACGCTGCTTTGAC	5344	ATCTTGCCTACCGGATCT
561	C	943_561_C_F_944_561_C_R	5312	GTCAAGAGAGCGCTATTGA	5345	AACAGGACAAACTGGCCAAC
561	D	945_561_D_F_946_561_D_R	5313	CCTCCAGCTTCAATAACCCA	5346	AAATCCCACTTCTCCTCGT
561	E	947_561_E_F_948_561_E_R	5314	TGTGTCCTCAGAGCCTCTAA	5347	GGAGGCCCTGCCATATCTATC
561	F	949_561_F_F_950_561_F_R	5315	CTGTGTTGGCTGGGTGATAA	5348	GGCAGCTGTTGTCGGTGATG
561	F	951_561_F_F_952_561_F_R	5316	GAGAGCACATCCTGGACCTC	5349	TTCATGCCGTGCTCCTTTGTC
561	F	953_561_F_F_954_561_F_R	5317	GCCACCAGAGATGGGGAAC	5350	TCTGCGTGATGTTGTCAC
561	F	955_561_F_F_956_561_F_R	5318	GTGGGCAAGGACGTGGTG	5351	CTCCCTTTGCTCCAGCGG
561	F	957_561_F_F_958_561_F_R	5319	CACGTCATCTTCTCTCAACGA	5352	GGAAGGACACAGGGCTTAC
561	G	1532_561_G_F_1533_561_G_R	5320	ACCGAATGATCTCGTTTCCA	5353	AAACTCACCTCTGCCCTT
561	G	1534_561_G_F_1535_561_G_R	5321	CACCCCCACAAGATGTTACC	5354	AGTGATCAGGGCTGGAAGAG
561	H	961_561_H_F_962_561_H_R	5322	GGCTCCCACTTGCAGGAC	5355	TGATTTGGGGTGCAGGCTCTC
561	H	963_561_H_F_964_561_H_R	5323	ACTCTGCAGTTGCTGCCGT	5356	CTGTGGCTGTGCACAGAT
561	H	1536_561_H_F_1537_561_H_R	5324	CACGCCAGATGGATGAG	5357	GACTGAGGAGCCACCGAG
561	I	967_561_I_F_968_561_I_R	5325	GTAGCTGAAGGTGGCCCTG	5358	CCACCAGGAGGATGGTGT
561	J	969_561_J_F_970_561_J_R	5326	TGTAGATGCCGGGAGGAG	5359	AGCTACTCTGGGACCGGAG
561	K	971_561_K_F_972_561_K_R	5327	ATGCTGGCGAGACTTAACGAC	5360	TTTGCTTAGCGGAAATGCT
561	L	973_561_L_F_974_561_L_R	5328	CACGCTCCTCAGTTAGGCTC	5361	CACCTTGATGATCTGGCCTT
561	L	975_561_L_F_976_561_L_R	5329	AGACCGCCTTCTCCAGACT	5362	GTCGATAACCTGTTGCCAGT
561	M	977_561_M_F_978_561_M_R	5363	CTGAACCAATCAATTACAGTCT	5366	GATMAATGCACAGGGGAAGTCT
561	N	979_561_N_F_980_561_N_R	5364	AGGGGAACACCGCTAAGTTT	5397	GTTGGTGTACACGAGGGGAAG
561	O	1538_561_O_F_1539_561_O_R	5365	TTCTCAATAGTAAGGGAAGCA	5398	ATGACGTTTCATGCCCAATTT
561	P	983_561_P_F_984_561_P_R	5366	TCCTTTAGCCAAAGCAAGATG	5399	ATATGGCAGAACGGGACAGA
561	Q	1248_561_Q_F_1249_561_Q_R	5367	CCAAGGGCTTCTCAAGCATA	5400	ACACTGGCCCGGTTAAAGTA
561	X	1744_561_X_F_1745_561_X_R	5368	GCCCCCTAAGTATACAGAGGAA	5401	AAGGAGGCAGACAGCAAAAA
561	Y	1746_561_Y_F_1747_561_Y_R	5369	GGAGCTCCTAACCACTGCAC	5402	CTTCCAGTTGTTCTCTCCT
561	Z	1748_561_Z_F_1749_561_Z_R	5370	AGAGGAAGCAACGGATACCA	5403	TCACACCGAAGCTTCACAAAGA
561	R	1957_561_R_F_1958_561_R_R	5371	ACCTGCCACGATAGCACAG	5404	ATAGGTGAGGAGGAACGTTGGC

214	B	192_214_B_F_193_214_B_R	5372	CACTGTGTTAAACGCTGG	5405	GTTGGATTACAGGCACGAG
214	B	194_214_B_F_195_214_B_R	5373	CAGAAGCAACCCACATGACC	5406	ACTACAGGTTTGACACCACA
214	A	196_214_A_F_197_214_A_R	5374	GCCCTTAGGGAGAGCAGC	5407	CCACATCGTGCCTTTGTA
214	C	626_214_C_F_627_214_C_R	5375	ATGCTCTCCTGATGGCTCCT	5408	AGGGAATGCAGGTGCMAAG
214	C	628_214_C_F_629_214_C_R	5376	ACTCGGAAAGGAAGGCTCT	5409	CATACCTTGAGTGCACACCG
214	AA	1607_214_AA_F_1608_214_AA_R	5377	AGACAGTGTGTTCCCGGAG	5410	TCACCTGCTCACCCACGTTAG
214	E	1609_214_E_F_1610_214_E_R	5378	ATATGTTTGGCTGGCTTTGGG	5411	GAAAGAGTGAAGCCGGTAACA
214	E	1611_214_E_F_1612_214_E_R	5379	CTGCTTCAAGATGCCAGTGA	5412	AACAACGCCCTGGGTTGAG
214	E	1613_214_E_F_1614_214_E_R	5380	CCGTCGCCAGGATACCTTTTC	5413	CCCAGGCTGTGTGTCCTTA
214	E	1615_214_E_F_1616_214_E_R	5381	ACACCCATCACCTTACATGG	5414	AATGAACGTGGTGACTACAGC
214	E	1617_214_E_F_1618_214_E_R	5382	TATCTGACGTGGTGTGC	5415	AGCAGAGTGAACAGTGGCTG
214	AA	1599_214_AA_F_1600_214_AA_R	5383	CGGGCGTGTATATCTTTCA	5416	TTCGCTGTGATCATGTGCG
214	AA	1601_214_AA_F_1602_214_AA_R	5384	TGTACGAACAGTCCACAGCAG	5417	GCCATGGTTGTTAAATTAGGC
214	AA	1603_214_AA_F_1604_214_AA_R	5385	CGACATGATCACCAAGCGAAA	5418	TTTGGTCTGCTTCAGTGGTG
214	AA	1605_214_AA_F_1606_214_AA_R	5386	CGAATAAAGGCGTCGAGAAG	5419	CAGGCTCCTCTTCAGAGTCG
224	W	133_224_W_F_134_224_W_R	5387	CACCTGTACCTCGCCTTTGTA	5420	GGGACCCACCTTGCTGAG
224	BB	1432_224_BB_F_1433_224_BB_R	5388	CCCAGCCCCCTTCTCACTG	5421	GGAAAAAGGGAACCTGGGAAGT
224	C	1434_224_C_F_1435_224_C_R	5389	CAGCAAGTCCCTCCTGATGT	5422	TTTAGCTTCCCTCCCTCAG
224	D	1436_224_D_F_1437_224_D_R	5390	GCAGATCCACAGGAAGAACAA	5423	AGCTGCCACCCCTCTATCTA
224	J	1438_224_J_F_1439_224_J_R	5391	TGTGGGGTACAGTGGCATTAA	5424	GCAAAACCACTCACCTCT
224	L	1440_224_L_F_1441_224_L_R	5392	ATCCAGAGATACCCACGCT	5425	CAAAAGTGTTCTGCGAGT
224	Y	1442_224_Y_F_1443_224_Y_R	5393	GCCTGTGGGTATTTTGCAC	5426	ACCTACCCCAACTTGTGACG
224	Z	1444_224_Z_F_1445_224_Z_R	5394	TTGATTGGATTTGAGCTCTGC	5427	CCGTGAGAGACACCTTCAC
224	S	131_224_S_F_132_224_S_R	5395	TTGGCAGACAGAAAGAGGAGG	5428	TTTCTGTAGGTCCATGAG
422	C	1859_422_C_F_1860_422_C_R	5429	TTATCTGGGACAGGTTGTGT	5462	CCCATTCAGAGGAGTGAGA
422	D	1861_422_D_F_1862_422_D_R	5430	CTGGCAGACCCGATTTGAAC	5463	GGCAGGCACCTCCAAATTTTC
422	E	1863_422_E_F_1864_422_E_R	5431	GTGAGGGCTGACCTATTGCT	5464	CGGCCCTACTGAGAACCAACT
422	F	1865_422_F_F_1866_422_F_R	5432	TTCTTTTGGCCCCAGATTGT	5465	TGAGATGAGGCAGATAGAGGTG
422	F	1867_422_F_F_1868_422_F_R	5433	AAGGCACACAAAGAACCTGGA	5466	AGGTGGCATCACTGCATC
436	A	1549_436_A_F_1550_436_A_R	5434	CCTAGAGGGTCACTGTTCCC	5467	TCGTACTCGAACAGGAAGGC
436	A	1551_436_A_F_1552_436_A_R	5435	ACCCAGACCCGACTAGGGGAC	5468	GACCCGAGGCCAGGATGAG
436	B	1553_436_B_F_1554_436_B_R	5436	TTCCCCATCAATTCAATTC	5469	TCAGGCCACGTCATCATTTA
436	C	1555_436_C_F_1556_436_C_R	5437	TTTCTTGGCTCTCCGTGAGT	5470	GAGCGAAAAAGGATCCACG
436	D	1557_436_D_F_1558_436_D_R	5438	GCCACGTGACCTTCTTTTC	5471	GGGTCAATGTGAAGAAATTGG
436	E	1559_436_E_F_1560_436_E_R	5439	TAGGAGACCCCTGTGACAT	5472	TGAGGCACAGAAAAATCACTTG
436	F	1561_436_F_F_1562_436_F_R	5440	CTGCACTCGAGGTGACAGAG	5473	ACACCTGGCCACCACTTACT
436	G	1563_436_G_F_1564_436_G_R	5441	TCTCTGAGGTTTTCGTGCT	5474	GGGATGAGCAGCAGAGACAC
436	H	1565_436_H_F_1566_436_H_R	5442	CAGGTGCTGAGGAAAGCCT	5475	TGCCTGAGTGTGTGCTTTC

436	I	1567_436_I_F_1568_436_I_R	<u>5443</u>	TGTGCCAGCTCCACTCTAAC	<u>5476</u>	ATGTCAAAATTTCCCTGCCTG
436	J	1569_436_J_F_1570_436_J_R	<u>5444</u>	GCCCCGTGCAGAAACACTTT	<u>5477</u>	GGTCTTGAGAGGGAAGGT
436	K	1571_436_K_F_1572_436_K_R	<u>5445</u>	CCATTCCGGTAAAGATTCCA	<u>5478</u>	ACACCCAAGAGATGAGAGG
436	L	1573_436_L_F_1574_436_L_R	<u>5446</u>	CTACTTCAGTGCACTTGCG	<u>5479</u>	ATTTCCTGGGGTGATGTG
436	M	1671_436_M_F_1672_436_M_R	<u>5447</u>	CCATCAGTGTGCTGAGTGCT	<u>5480</u>	ACAGGCCCTTAAATTGCCA
449	A	1971_449_A_F_1972_449_A_R	<u>5448</u>	CCAGATATTCACAGCCTCAGC	<u>5481</u>	ATCAGTGCCATCTCTGTCCC
449	A	1973_449_A_F_1974_449_A_R	<u>5449</u>	CTGGGTAGAGAGCCTGGCTAT	<u>5482</u>	AAATGCTCCTGCCTCAGAAA
449	A	1975_449_A_F_1976_449_A_R	<u>5450</u>	GGAAGAGGTGCTAGACGCTG	<u>5483</u>	GCTAGTGGGATGGGTAATT
449	B	1977_449_B_F_1978_449_B_R	<u>5451</u>	AGTGGGCTCAGGGTGAC	<u>5484</u>	TCCTGCTCCATCTCAGGT
449	B	1979_449_B_F_1980_449_B_R	<u>5452</u>	ATGTGGCAAGCCAGGAC	<u>5485</u>	CCCCAAGCATAGGACACAGA
449	C	1981_449_C_F_1982_449_C_R	<u>5453</u>	TCAATCCCCAATCTTCTCT	<u>5486</u>	CTCTTCCCTCTCCTTGCC
449	D	1983_449_D_F_1984_449_D_R	<u>5454</u>	CAACGCCATCTTACACAGA	<u>5487</u>	TGTGAGTGTGTAGTACTTGTTCC
449	D	1985_449_D_F_1986_449_D_R	<u>5455</u>	ACTGTGATGACCTGCTCCT	<u>5488</u>	TGTGTGTGTGGAGGTC
449	E	1987_449_E_F_1988_449_E_R	<u>5456</u>	CAAACCATTTATGAGCCTGGG	<u>5489</u>	GTGTTCTGACCTTCAAGCC
449	F	1989_449_F_F_1990_449_F_R	<u>5457</u>	TGTGAGCTTAACACCTCTCCTTC	<u>5490</u>	TGAGTGTGGAGAAGATCCC
449	F	1991_449_F_F_1992_449_F_R	<u>5458</u>	GCTCCTTAGCCAAATATGGGA	<u>5491</u>	ATAGATCCCCAGACCCAAAC
449	F	1993_449_F_F_1994_449_F_R	<u>5459</u>	ATTCCAAAGGCCAAGTCTCTG	<u>5492</u>	TCTGGCCTGGGATAACTCAT
449	F	2011_449_F_F_1992_449_F_R	<u>5460</u>	CAGGTGCTCTTAGCCAAATA	<u>5493</u>	ATAGATCCCCAGACCCAAAC
515	A	1226_515_A_F_1227_515_A_R	<u>5461</u>	GCTCCATCGGACTCACTAGC	<u>5494</u>	TGGATTTCCAGGACTTGAGG
515	A	1228_515_A_F_1229_515_A_R	<u>5495</u>	TGTTGGGGCTGGAGTTTATC	<u>5528</u>	TCAATGGCAACATGAAGAGC
515	A	1230_515_A_F_1231_515_A_R	<u>5496</u>	GCCGTTCTGTGATGAGTACT	<u>5529</u>	GCCATTCTGATCAGCAACT
515	A	1232_515_A_F_1233_515_A_R	<u>5497</u>	CAGCCATCATCTCTTGCTT	<u>5530</u>	CCACCATGATGAAGGTGATG
515	A	1234_515_A_F_1235_515_A_R	<u>5498</u>	GCATCATCTCTGTTCTGCTCA	<u>5531</u>	TGATAAAGAACGCCAGGTCC
515	A	1236_515_A_F_1237_515_A_R	<u>5499</u>	GGCCATCGTCTTTGTGCTATCT	<u>5532</u>	GCTGTGCTGCGGTTATTAT
515	A	1238_515_A_F_1239_515_A_R	<u>5500</u>	ACTTCTCCAGCCCATCTCTT	<u>5533</u>	GCAACAGCCCAACTGTTTCT
515	A	1240_515_A_F_1241_515_A_R	<u>5501</u>	CATGGAGCCCTCTTATCTG	<u>5534</u>	GCAACCACTCTCCACTCAT
570	C	1310_570_C_F_1311_570_C_R	<u>5502</u>	GGTTTTCATCCTTGAAGACTGT	<u>5535</u>	CCACAGAGGAAGACCACAA
570	C	1312_570_C_F_1313_570_C_R	<u>5503</u>	TAGCGCGCATTTGCCATATAT	<u>5536</u>	ACCTTTCAACAGGCCCAAGA
570	D	1314_570_D_F_1315_570_D_R	<u>5504</u>	TGAGCTGGTTTCTTACCTCCA	<u>5537</u>	CAAAAGCCAAAGAAACAGGGA
570	D	1316_570_D_F_1317_570_D_R	<u>5505</u>	AGGCATTGGAGCTTTTCAGC	<u>5538</u>	AAATGGCCAAAGCAAGTGCT
570	E	1318_570_E_F_1319_570_E_R	<u>5506</u>	GAGAGCACAGTTGTCACAA	<u>5539</u>	ACAATGCTTTTGTGTGGGTG
570	F	1320_570_F_F_1321_570_F_R	<u>5507</u>	CCTGTATTGCGGGGAGTAAA	<u>5540</u>	TCTGAATCCACAACACTGTGC
570	G	1322_570_G_F_1323_570_G_R	<u>5508</u>	CGAAGTCTCGTAGCCACATC	<u>5541</u>	GTGCTGGACTCAGACACCT
570	H	1324_570_H_F_1325_570_H_R	<u>5509</u>	CCATGTGTTAAAGTGCCCT	<u>5542</u>	CCCCTCACTGGCTATTITCA
570	I	1326_570_I_F_1327_570_I_R	<u>5510</u>	GCTTGATCACTGTGTTTCC	<u>5543</u>	AGAAAGGGAAGCTTGGGGTA
570	I	1516_570_I_F_1517_570_I_R	<u>5511</u>	GGGACGTCTTGCACAGACA	<u>5544</u>	TGGAGCTGTTTTTGTGCATC
570	J	1330_570_J_F_1331_570_J_R	<u>5512</u>	AAAATACCTGTAGCAGCGCA	<u>5545</u>	ATTGGCTTGTATCGCTGA
570	J	1332_570_J_F_1333_570_J_R	<u>5513</u>	GCTACCTCTCTGCTTTTCT	<u>5546</u>	ATCAATCCAGGCAACATGTC

570	B	1897_570_B_F_1898_570_B_R	<u>5514</u>	TGTCGTATTCTCGTAACGGG	<u>5547</u>	GCCGTGCAGTTGAGCAGG
581	C	1362_581_C_F_1363_581_C_R	<u>5515</u>	TTCCGTGACTCTGGATCTT	<u>5548</u>	ATGAACCTCAACACCAAGG
581	D	1364_581_D_F_1365_581_D_R	<u>5516</u>	GGAAMACCTTGCTGTGGAA	<u>5549</u>	TGTTGGAACAGACCTGATTTTC
581	E	1366_581_E_F_1367_581_E_R	<u>5517</u>	TGAGGGGAGAGATACAGGTGA	<u>5550</u>	TGTTGCCACACAAACAATG
581	E	1368_581_E_F_1369_581_E_R	<u>5518</u>	ACAAGATGTGCCTAACGTGGC	<u>5551</u>	GACTCCGCTTTGGGAAAA
581	F	1370_581_F_F_1371_581_F_R	<u>5519</u>	ACCATGCCCTTGCCAAGAA	<u>5552</u>	GCCTATACTGTGCTGCCAAA
581	F	1524_581_F_F_1525_581_F_R	<u>5520</u>	CAGTACTACGACATTTCTGCCAA	<u>5553</u>	GGAATTAACAAGCCAAACCG
581	G	1374_581_G_F_1375_581_G_R	<u>5521</u>	GATTGTTGGTTGGCTTGT	<u>5554</u>	TCAGCATCCACAGATGAAG
698	A	1334_698_A_F_1335_698_A_R	<u>5522</u>	GACCAGAAATCCCAAGAGAC	<u>5555</u>	TGCTGTGATTGCCCTAACA
698	B	1336_698_B_F_1337_698_B_R	<u>5523</u>	TTTGGCCACTGAGATGCTA	<u>5556</u>	AAATCCAGTGGCTTCTCC
698	C	1338_698_C_F_1339_698_C_R	<u>5524</u>	ACTGCTTTGTCTCTGGGAA	<u>5557</u>	CACAAAACGAAACCTGCGC
698	E	1342_698_E_F_1343_698_E_R	<u>5525</u>	TGTTTGGCTGATCAGTGA	<u>5558</u>	TGACTGCCAAGCAATTTCA
698	F	1344_698_F_F_1345_698_F_R	<u>5526</u>	AGGAAGGTGTTTATGACCG	<u>5559</u>	GCCTTTACCCGAAACCTGC
698	G	1520_698_G_F_1521_698_G_R	<u>5527</u>	CAGGTGAGTTAGTTCTCTGCC	<u>5560</u>	CCTCCATCTTGCACTTCAT
698	G	1522_698_G_F_1523_698_G_R	<u>5561</u>	TCAGGTGCTGCTGTTGTCA	<u>5594</u>	AAACGGCATCTACCAATTAATC
698	H	1348_698_H_F_1349_698_H_R	<u>5562</u>	CATCCCGGTGAGTTGATTT	<u>5595</u>	CTCACTGCCACCCACAGTAG
698	I	1350_698_I_F_1351_698_I_R	<u>5563</u>	TCCTGCTCCTCTGTGTAAGG	<u>5596</u>	TTTCTGGAAGACCCCAATTT
698	J	1352_698_J_F_1353_698_J_R	<u>5564</u>	TGTGCTGATGAGCATGAATTG	<u>5597</u>	CCCTCATCTCTTCACTCTGTG
698	K	1354_698_K_F_1355_698_K_R	<u>5565</u>	GGAGCATGTGAACACCTGAA	<u>5598</u>	GAAACCAACCAACCAAGAGAA
698	L	1356_698_L_F_1357_698_L_R	<u>5566</u>	AGTTTTCAGCACATCCGTGT	<u>5599</u>	GCCTTTAAACCAACAGCTATTTTC
698	M	1358_698_M_F_1359_698_M_R	<u>5567</u>	TTGACCTACAAGCTGTGCCA	<u>5600</u>	CTCTGGCCAAACAAGAAAGC
698	M	1360_698_M_F_1361_698_M_R	<u>5568</u>	TCCTTCCACTAAGGGGTCA	<u>5601</u>	TCCTAATCCCTTCCCAAGT
698	D	1518_698_D_F_1519_698_D_R	<u>5569</u>	TGTGCTCTCTGCTGTCTCT	<u>5602</u>	ACCATTTGTTATTCGGGGCT
702	A	630_702_A_F_631_702_A_R	<u>5570</u>	GGCCAGGGACATCAGGTT	<u>5603</u>	GTCTGCAGCTGCCCTGTT
702	A	632_702_A_F_633_702_A_R	<u>5571</u>	CCCTTCACCCCTGCTCTCT	<u>5604</u>	CATAAGACGGAGCTGTGCT
702	B	634_702_B_F_635_702_B_R	<u>5572</u>	AGTGAGCTGGGCTAGGCTCT	<u>5605</u>	GGAGACCCCGTTCTCTCAC
702	C	636_702_C_F_637_702_C_R	<u>5573</u>	CTGCTCCTCATCTCACAGG	<u>5606</u>	CCCTGAACCTTCACGAGGT
702	C	638_702_C_F_639_702_C_R	<u>5574</u>	GTCGAAGGGGTAGCCGTC	<u>5607</u>	CCTGTTCTCCGTGACTCACTC
702	D	640_702_D_F_641_702_D_R	<u>5575</u>	GGGGTTCTGACCCCTCTT	<u>5608</u>	CAGTGGCTGTCCACGAGTT
702	D	642_702_D_F_643_702_D_R	<u>5576</u>	ACCTTGTCTCTGATGGGAG	<u>5609</u>	GCCCTTCTTGCCCTTAGTTTC
702	E	644_702_E_F_645_702_E_R	<u>5577</u>	CAGAGCCTGCTCTGAGGTG	<u>5610</u>	GGACAGGGATGAGACAGAC
702	F	646_702_F_F_647_702_F_R	<u>5578</u>	CACACAAGGATGCCGTCTC	<u>5611</u>	GGTCTGCACCCAGAGTGG
702	G	648_702_G_F_649_702_G_R	<u>5579</u>	TGGGTGCAGACCGTCTCT	<u>5612</u>	CTCCATGAGGGGAGACAGA
702	H	650_702_H_F_651_702_H_R	<u>5580</u>	CTTGCTGCCCTGTAGTGAT	<u>5613</u>	CATGACGCTGCCTTCTC
702	H	652_702_H_F_653_702_H_R	<u>5581</u>	CCTCGTGTGTCATCGTAA	<u>5614</u>	GGCTGACACAGGAGAAGGAA
702	I	654_702_I_F_655_702_I_R	<u>5582</u>	CGAGGGTACCCACTCCCAT	<u>5615</u>	ACCAACCCCAACCCACACT
702	I	656_702_I_F_657_702_I_R	<u>5583</u>	AGCAGGGAGAGGTATGTTG	<u>5616</u>	CAGAAAGGTGCCCAGTCA
702	I	658_702_I_F_659_702_I_R	<u>5584</u>	CCGAGATGCTCCCTCAG	<u>5617</u>	CACAGAGGGCAAGGACTGTG

702	I	660_702_I_F_661_702_I_R	<u>5585</u>	TCGTCAGTCAACACAGTCCC	<u>5618</u>	CCAGGCCCTGACGCTATG
702	I	662_702_I_F_663_702_I_R	<u>5586</u>	CACAGTCCTGGCCCTCTGTG	<u>5619</u>	GCCCTCCAGGACACACAT
702	I	664_702_I_F_665_702_I_R	<u>5587</u>	GTCGATGAGCAGACCTCGTA	<u>5620</u>	TGCCCTCTACTTCTCCGTG
702	I	666_702_I_F_667_702_I_R	<u>5588</u>	CTCCACACACCAGCCAGTC	<u>5621</u>	CAGCTTGTCGAAGCCCC
722	B	382_722_B_F_510_722_B_R	<u>5589</u>	TTGAGTTGCGTAATTTGTGCC	<u>5622</u>	GGACAGGTAGGCAGGCTATG
722	C	813_722_C_F_814_722_C_R	<u>5590</u>	GATTTGAGTTTGCCATGCTGT	<u>5623</u>	ACAGCCAGAGGGACACACA
722	D	386_722_D_F_387_722_D_R	<u>5591</u>	ATGTTGATATTATAGCTCAGATGC	<u>5624</u>	CAATACCCATTAATCCCAACATC
722	E	388_722_E_F_389_722_E_R	<u>5592</u>	TTGAAGTCAGGCTTGGACA	<u>5625</u>	TTGAGAGTCTGCAAGAAGAAAGT
722	F	390_722_F_F_391_722_F_R	<u>5593</u>	ATGGCCCTCAGATACGAATG	<u>5626</u>	TTGAAGTGAGACCTTAAGGAGAGA
722	G	512_722_G_F_513_722_G_R	<u>5627</u>	ATGGTTGCAAAATGCGTTTGT	<u>5652</u>	ACAGAAAGAGGACATGGAGCC
722	H	394_722_H_F_395_722_H_R	<u>5628</u>	CCCTTTAACTTCCAACCACA	<u>5653</u>	TCTTGGAGAAATGCAAGAGTCTG
722	I	396_722_I_F_397_722_I_R	<u>5629</u>	CCATTACATGCACATCGTGT	<u>5654</u>	TCTTCGAAGCCAAACTCACC
722	J	1526_722_J_F_1527_722_J_R	<u>5630</u>	GCAAAATGCCATTGTTGATTT	<u>5655</u>	CGGGTTACAGCGCTGAGAT
722	AA	739_722_AA_F_740_722_AA_R	<u>5631</u>	TCAGCTTGCTTTTCTTGACA	<u>5656</u>	GTGGCTGGCAAGCTTTTATT
722	A	1901_722_A_F_1902_722_A_R	<u>5632</u>	GGGCTCCCGCTGGAAAG	<u>5657</u>	GGCCTGAACCGCTAACCC
748	A	1995_748_A_F_1996_748_A_R	<u>5633</u>	TAGCATCCACCTGTGTCCTCC	<u>5658</u>	CAGAAAGCCAGAAAGGGCAAAG
748	A	1997_748_A_F_1998_748_A_R	<u>5634</u>	GCTTCATGCTTGTGCTTAAAA	<u>5659</u>	TGCCTTTCAATCAGTAGAAGAAC
748	A	1999_748_A_F_2000_748_A_R	<u>5635</u>	TAAGAATGGTTTCGAGGGTG	<u>5660</u>	TGGTTGAGAGCAAGAGAGGAA
751	U	1945_751_U_F_1946_751_U_R	<u>5636</u>	GGTGCTACCTCTCTGATCCT	<u>5661</u>	CACCTGCAGCCTCATGTGTA
751	V	1947_751_V_F_1948_751_V_R	<u>5637</u>	TAGCCTGTGTTGAGGGCAGT	<u>5662</u>	TCCTGTGACCTCAAAAGCATCC
751	W	1949_751_W_F_1950_751_W_R	<u>5638</u>	TGCCACTCAGGGTGACTGT	<u>5663</u>	TGCAAGCCTGCTCCTGAT
751	X	1951_751_X_F_1952_751_X_R	<u>5639</u>	CCTAACTACGTGCCAAAGGGC	<u>5664</u>	GCTCAGGATTTGAGTCCACAG
751	Y	1953_751_Y_F_1954_751_Y_R	<u>5640</u>	ATTCCAATCCCAACCTCC	<u>5665</u>	CTGGAGCCCTCGGTTTATG
751	Z	1955_751_Z_F_1956_751_Z_R	<u>5641</u>	TCACTGGGCTTATGGCTCTC	<u>5666</u>	GTCCATGAGCAAAAGGTGGAG
848	Y	2001_848_Y_F_2002_848_Y_R	<u>5642</u>	GCCTCCAACCTTGGCTCTC	<u>5667</u>	TAAACGCCAAATCCACCTC
848	Y	2003_848_Y_F_2002_848_Y_R	<u>5643</u>	TCTCTCGCCCTCTCTCTG	<u>5668</u>	TAAACGCCAAATCCACCTC
848	Z	2004_848_Z_F_2005_848_Z_R	<u>5644</u>	CATTGTCTTCACTGGCCG	<u>5669</u>	TGGTGTCTGCGCGTGATT
GenR2	A	1453_GenR2_A_F_1454_GenR2_A_R	<u>5645</u>	CCAAGCCCCAAATTTAAGTG	<u>5670</u>	CCTCTCGCCTAAACCTGTGC
GenR2	B	1455_GenR2_B_F_1456_GenR2_B_R	<u>5646</u>	CATTTCCTGGCACACAATGG	<u>5671</u>	TGGTTGAGCCACCATACTCA
GenR2	C	1457_GenR2_C_F_1458_GenR2_C_R	<u>5647</u>	TATTTCACCCAGAGGTTG	<u>5672</u>	TGTTGCCAAGAATGTGGAAA
GenR2	D	1459_GenR2_D_F_1460_GenR2_D_R	<u>5648</u>	TCCTCTCAGGAACAGAGCCA	<u>5673</u>	ATGCACCTCAGCGACCTTCTC
GenR2	F	1575_GenR2_F_F_1576_GenR2_F_R	<u>5649</u>	GTCCTTCCCATCCCTCAACA	<u>5674</u>	GGGAGGCATTAATGAACCAGA
GenR2	F	1577_GenR2_F_F_1578_GenR2_F_R	<u>5650</u>	TAGCGCCCTATCCCTTCTT	<u>5675</u>	TCCATCCCAAGCTTCACTCT
GenR2	E	1790_GenR2_E_F_1791_GenR2_E_R	<u>5651</u>	CTCTGACCTTGACCTACCCC	<u>5676</u>	CCACCGTGTCTTCAAAATTCA

Please replace Table 9 on pages 178-181 with the following table:

PLEASE SEE NEXT PAGE FOR TABLE

TABLE 9: SEQUENCING PRIMERS

Gene	Exon	Forward Primer	Forward Sequence	SEQ ID NO.	Reverse Primer	Reverse Sequence	SEQ ID NO.
454	B	MDSseq_118_454_B_F	CCAGATACTGGGCAAGGAG	5677	MDSseq_118_454_B_R	GCACCAGACATGAGGCTAT	5703
454	E	MDSseq_119_454_E_F	AGCCAGCAGAATCCACAGTC	5678	MDSseq_119_454_E_R	GGTACCCTGGAAAGATCTGGG	5704
454	E	MDSseq_473_454_E_F	TCCTGTTACTCTCCTGCGGT	5679	MDSseq_473_454_E_R	CCAACCTCAGCAGCAAGAATGA	5705
454	F	MDSseq_120_454_F_F	ACAGCAAGGAGGAAGTCCG	5680	MDSseq_120_454_F_R	TGGAAGAAGGTTCTCCAGC	5706
454	G	MDSseq_121_454_G_F	TTCTCCCAAGCAAGTGACC	5681	MDSseq_121_454_G_R	CCACAGGAAAGGAATACACCA	5707
454	H	MDSseq_122_454_H_F	AGTGCCCTGAATTCACAGTCT	5682	MDSseq_122_454_H_R	CATTCACTTGTGCTTGG	5708
454	H	MDSseq_291_454_H_F	AGTGCCCTGAATTCACAGTCT	5683	MDSseq_291_454_H_R	CATTCACTTGTGCTTGG	5709
454	K	MDSseq_123_454_K_F	CCCAGAACCCACGACATTTC	5684	MDSseq_123_454_K_R	TAGAAATTGCTTTCAGGCCC	5710
454	L	MDSseq_124_454_L_F	GTCTCCCTTAATGTGTGGG	5685	MDSseq_124_454_L_R	GGGCTAATTTTCTGTCAT	5711
454	M	MDSseq_125_454_M_F	CCAGCAGCTTGAACGCATCTA	5686	MDSseq_125_454_M_R	CTTCCCTCTATCTTGCCCC	5712
454	N	MDSseq_126_454_N_F	AGCATGGGGTCCCAATTT	5687	MDSseq_126_454_N_R	ATTGGAAGGGGGCATAAAG	5713
454	O	MDSseq_127_454_O_F	CGATTCCCTGGACCAACCAGA	5688	MDSseq_127_454_O_R	GGACAGTTTGTCTGTGCTC	5714
454	O	MDSseq_128_454_O_F	GAACACATGCATGTCTCTGA	5689	MDSseq_128_454_O_R	ACAGACAGCATTTGCGCTTG	5715
454	AA	MDSseq_460_454_AA_F	CTCAACTCCACTTTCTCTCGG	5690	MDSseq_460_454_AA_R	CAAGAACCGCCCAAGTCTTAC	5716
454	AA	MDSseq_470_454_AA_F	TGCATCTTTGAGTACTGCTG	5691	MDSseq_470_454_AA_R	ACTCTGCTCTGCAGTTGGTG	5717
454	AA	MDSseq_471_454_AA_F	TCTTGACATTTGCAAGGC	5692	MDSseq_471_454_AA_R	TCAGAAATGTGCACCTGAAGC	5718
757	A	MDSseq_407_757_A_F	CTCGCTTCCCGGTAATTGTT	5693	MDSseq_407_757_A_R	GCCTTCATGACACAGGTAGTT	5719
757	A	MDSseq_408_757_A_F	TTCTTCCTGTGCTCGCTGTA	5694	MDSseq_408_757_A_R	CTCTCCAGTCCCTCCTGAT	5720
757	A	MDSseq_409_757_A_F	CGTGACGTGTACTGGAGC	5695	MDSseq_409_757_A_R	CTCCAGCTTTGTCGCTGTTCT	5721
757	A	MDSseq_410_757_A_F	AGCCAACAGCAGCTACTTCC	5696	MDSseq_410_757_A_R	GACTGGGCGAGGATCTCATA	5722
757	A	MDSseq_411_757_A_F	TCTTATGCTGCTGCTGTG	5697	MDSseq_411_757_A_R	GGGTCTCTCTTTCCTCTGC	5723
757	A	MDSseq_412_757_A_F	AGGGAAGCTCTCCAGTGA	5698	MDSseq_412_757_A_R	TCTGCCAACCTAGTGGTCC	5724
757	A	MDSseq_413_757_A_F	TGAACCTCAACGATGTGCA	5699	MDSseq_413_757_A_R	TTCCAACCTTACACATTGCC	5725
757	A	MDSseq_418_757_A_F	CTCGCTTCCGGTATTGTT	5700	MDSseq_418_757_A_R	GCCTGCATGCACAGGTAGTT	5726
757	A	MDSseq_419_757_A_F	AGGGAAGCTCTCCAGTGA	5701	MDSseq_419_757_A_R	TCTGCCAACCTAGTGGTCC	5727
757	A	MDSseq_421_757_A_F	CAAACTTGTGCTCTCCG	5702	MDSseq_421_757_A_R	AGTTGGGCTGTTCTTGTG	5728
757	A	MDSseq_422_757_A_F	CAAGAAGAGGCGGAAGTTTG	5729	MDSseq_422_757_A_R	TACAGCGAGCACAGGAAGAA	5761
757	A	MDSseq_423_757_A_F	GAGGACACGTCACACGCC	5730	MDSseq_423_757_A_R	CTCGTCCGAGCCGTTGTT	5762
757	A	MDSseq_424_757_A_F	CAAGAAGAGGCGGAAGTTTG	5731	MDSseq_424_757_A_R	TACAGCGAGCACAGGAAGAA	5763
757	A	MDSseq_425_757_A_F	GAGGACACGTCACACGCC	5732	MDSseq_425_757_A_R	CTCGTCCGAGCCGTTGTT	5764
561	B	MDSseq_169_561_B_F	ACTGCTCTCCCGTGAAAGTG	5733	MDSseq_169_561_B_R	CCATCAGCATCTGTGTGACC	5765

561	C	MDSeq_170_561_C_F	TTAAGCCAAAGGAAGAGACA	<u>5734</u>	MDSeq_170_561_C_R	CCTGATGGGATTGCTTT	<u>5766</u>
561	E	MDSeq_171_561_E_F	ATCTGTGTGTGAGCTGGC	<u>5735</u>	MDSeq_171_561_E_R	GGGTGTGAAAGACAAGAGC	<u>5767</u>
561	H	MDSeq_172_561_H_F	AAATGTTGACGTCACTGGC	<u>5736</u>	MDSeq_172_561_H_R	CTGTGGCTGTGGCAGGAT	<u>5768</u>
561	J	MDSeq_173_561_J_F	TGTTGGAGCTGAGAGACCTG	<u>5737</u>	MDSeq_173_561_J_R	CCTTAAACTCTTTTACCAGACC	<u>5769</u>
561	H	MDSeq_174_561_H_F	CTCTGGGCAAGGACTGGT	<u>5738</u>	MDSeq_174_561_H_R	TGACAGAGTCCACCAGCAAA	<u>5770</u>
561	M	MDSeq_177_561_M_F	ACCCTGCCTGATGAGAAGAA	<u>5739</u>	MDSeq_177_561_M_R	TGTTTGCAGCAAGACGGTA	<u>5771</u>
561	P	MDSeq_183_561_P_F	AGGCAGATTCTCAGCTCCT	<u>5740</u>	MDSeq_183_561_P_R	CAGAGGGCAAAATAACCTCA	<u>5772</u>
561	G	MDSeq_390_561_G_F	GCATTTCAGGAAGATGGTG	<u>5741</u>	MDSeq_390_561_G_R	TAATCCAGAGCAGAGCAGGG	<u>5773</u>
561	H	MDSeq_392_561_H_F	CTCTGGGCAAGGACTGGT	<u>5742</u>	MDSeq_392_561_H_R	TGACAGAGTCCACCAGCAAA	<u>5774</u>
561	X	MDSeq_401_561_X_F	GAACTGCCCTGTCCATCTGT	<u>5743</u>	MDSeq_401_561_X_R	AAATCTCAGGCTGGAGGAC	<u>5775</u>
561	Y	MDSeq_402_561_Y_F	ACAACCTCCAATTGGCGAGAA	<u>5744</u>	MDSeq_402_561_Y_R	CCAAGCAGAGATAACCAAGCA	<u>5776</u>
561	X	MDSeq_415_561_X_F	GAACTGCCCTGTCCATCTGT	<u>5745</u>	MDSeq_415_561_X_R	AAATCTCAGGCTGGAGGAC	<u>5777</u>
561	X	MDSeq_417_561_X_F	GAACTGCCCTGTCCATCTGT	<u>5746</u>	MDSeq_417_561_X_R	AAATCTCAGGCTGGAGGAC	<u>5778</u>
561	X	MDSeq_417_561_X_F	GAACTGCCCTGTCCATCTGT	<u>5746</u>	MDSeq_417_561_X_R	AAATCTCAGGCTGGAGGAC	<u>5778</u>
214	B	MDSeq_15_214_B_F	GACAGTCTGCTCCACATCCA	<u>5747</u>	MDSeq_15_214_B_R	TGGAGATGAAGTCTTGCTCT	<u>5779</u>
214	C	MDSeq_110_214_C_F	ATATGTTTGTGCTGGCTTGGG	<u>5748</u>	MDSeq_110_214_C_R	CCCAGGCTGTGTCTCTCTA	<u>5780</u>
214	E	MDSeq_343_214_E_F	TGCTTCTGTTTGTCACTGC	<u>5749</u>	MDSeq_343_214_E_R	TGAGGACACGATGAACCTGA	<u>5781</u>
214	E	MDSeq_383_214_E_F	ATGACCTGGGTGAGGACTT	<u>5750</u>	MDSeq_383_214_E_R	GCAGTGACAAACAGGAAGCA	<u>5782</u>
214	AA	MDSeq_399_214_AA_F	CGAATAAAGGCGTCGAGAAG	<u>5751</u>	MDSeq_399_214_AA_R	CCTTCTGAGAGGACGTG	<u>5783</u>
224	BB	MDSeq_403_224_BB_F	AATTGACTTTCCCGCCTTCT	<u>5752</u>	MDSeq_403_224_BB_R	GCCCAGCATCTTCTACTT	<u>5784</u>
422	E	MDSeq_431_422_E_F	AAGCATCTTTGGCGAAGTCAT	<u>5753</u>	MDSeq_431_422_E_R	AAAGGAGACACTGCCAGAA	<u>5785</u>
422	F	MDSeq_434_422_F_F	TGGCATCTCTGATGTACTTG	<u>5754</u>	MDSeq_434_422_F_R	GTGTGCATGCCTATGTCTC	<u>5786</u>
422	C	MDSeq_323_436_C_F	TGTGAAAAAGTGTGCTCTGAA	<u>5755</u>	MDSeq_323_436_C_R	AGTTGGGTGACAGAGCG	<u>5787</u>
422	D	MDSeq_324_436_D_F	TGTGAAAAAGTGTGCTCTGAA	<u>5756</u>	MDSeq_324_436_D_R	AGTTGGGTGACAGAGCG	<u>5788</u>
422	E	MDSeq_325_436_E_F	TCCTTAGCCTTGGCATCACCC	<u>5757</u>	MDSeq_325_436_E_R	ACGCAGAGTTGAAGGTGCTT	<u>5789</u>
422	G	MDSeq_326_436_G_F	CTGCACCTGAGGTGACAGAG	<u>5758</u>	MDSeq_326_436_G_R	AGCCAGGAGATACGTTGTGC	<u>5790</u>
422	K	MDSeq_327_436_K_F	GCTAGGCATGGTGAAGTGCT	<u>5759</u>	MDSeq_327_436_K_R	CGCAAGGTGCACCTGAAGTAG	<u>5791</u>
422	B	MDSeq_340_436_B_F	CCATCAGTGTGCTGAGTGCT	<u>5760</u>	MDSeq_340_436_B_R	ACCCAAAATGTGAAAAGGTG	<u>5792</u>
422	L	MDSeq_374_436_L_F	GCACAGGCGCTCTCATCTCTT	<u>5761</u>	MDSeq_374_436_L_R	AGAGTTGACCCAGCCAAAGAA	<u>5825</u>
422	A	MDSeq_375_436_A_F	CAAGATTCTCTCACCTCGG	<u>5762</u>	MDSeq_375_436_A_R	AACAGCAGCAAGCAGCCT	<u>5826</u>
422	C	MDSeq_393_436_C_F	TCACCTGTTTTCATTGGGTTA	<u>5763</u>	MDSeq_393_436_C_R	GTAGGGCAAGAGCTGGGATG	<u>5827</u>
422	D	MDSeq_394_436_D_F	TCACCTGTTTTCATTGGGTTA	<u>5764</u>	MDSeq_394_436_D_R	GTAGGGCAAGAGCTGGGATG	<u>5828</u>
422	G	MDSeq_395_436_G_F	GGCTGCAGAAAACTTCACTCT	<u>5765</u>	MDSeq_395_436_G_R	TGAGTGCTGTGCTTTCAGTGG	<u>5829</u>
422	A	MDSeq_396_436_A_F	GCTGGGATGACAGGTGTGAG	<u>5766</u>	MDSeq_396_436_A_R	TCCCAAAAGTGTGCGATTAC	<u>5830</u>
422	A	MDSeq_404_436_A_F	AGGAGCCCTTTCGCTCTCAA	<u>5767</u>	MDSeq_404_436_A_R	ATGTTGCCCAAAATTGGTTTC	<u>5831</u>
422	D	MDSeq_414_436_D_F	TCACCTGTTTTCATTGGGTTA	<u>5800</u>	MDSeq_414_436_D_R	GTAGGGCAAGAGCTGGGATG	<u>5832</u>
422	D	MDSeq_416_436_D_F	TCACCTGTTTTCATTGGGTTA	<u>5801</u>	MDSeq_416_436_D_R	GTAGGGCAAGAGCTGGGATG	<u>5833</u>
436	C	MDSeq_323_436_C_F	TGTGAAAAGTGTGCTCTGAA	<u>5802</u>	MDSeq_323_436_C_R	AGTTGGGTGACAGAGCG	<u>5834</u>

436	D	MDSseq_324_436_D_F	TGTGAAAAGTGTCTCTGAA	5803	MDSseq_324_436_D_R	AGTTGGGTGACAGAGCG	5835
436	E	MDSseq_325_436_E_F	TCATTAGCTTGGCATCACCC	5804	MDSseq_325_436_E_R	ACGCAGAGTTGAAGGTGCTT	5836
436	K	MDSseq_327_436_K_F	GCTAGGCATGGTGAAGTGTT	5805	MDSseq_327_436_K_R	CGCAAGGTGCACTGAAGTAG	5837
436	B	MDSseq_340_436_B_F	CCATCAGTGTGCTGAGTGCT	5806	MDSseq_340_436_B_R	ACCCAAATGTGMAAGGTG	5838
436	L	MDSseq_374_436_L_F	GCACAGGCGCTCTCATCTCTT	5807	MDSseq_374_436_L_R	AGAGTTGACCCAGCCAAAGAA	5839
436	C	MDSseq_393_436_C_F	TCAGTGTTTTCCATTGGGTTA	5808	MDSseq_393_436_C_R	GTAGGGCAAGAGCTGGGATG	5840
436	D	MDSseq_394_436_D_F	TCAGTGTTTTCCATTGGGTTA	5809	MDSseq_394_436_D_R	GTAGGGCAAGAGCTGGGATG	5841
436	G	MDSseq_395_436_G_F	GGCTGCAGAAAACCTTCACCT	5810	T MDSseq_395_436_G_R	TGAGTGTGTGCTTTCAGTGG	5842
436	A	MDSseq_404_436_A_F	AGGAGCCCTTTCGTCTCAA	5811	MDSseq_404_436_A_R	ATGTTGCCCAAAATTGGTTTC	5843
436	D	MDSseq_414_436_D_F	TCAGTGTTTTCCATTGGGTTA	5812	MDSseq_414_436_D_R	GTAGGGCAAGAGCTGGGATG	5844
436	D	MDSseq_416_436_D_F	TCAGTGTTTTCCATTGGGTTA	5813	MDSseq_416_436_D_R	GTAGGGCAAGAGCTGGGATG	5845
449	D	MDSseq_462_449_D_F	GTCACACAGCCAGTAGGCGAG	5814	MDSseq_462_449_D_R	CAGAGAGCAAGAAAGGCCAAG	5846
449	F	MDSseq_463_449_F_F	AAGAGAAAATCCGAGAGACC	5815	MDSseq_463_449_F_R	ACGGGGTCTCCCTGTGATA	5847
449	A	MDSseq_472_449_A_F	CCAACCTTCAGTTTCCCAACG	5816	MDSseq_472_449_A_R	CAGGAGCTGGAGCTTGATA	5848
449	F	MDSseq_474_449_F_F	CACATATCTGCCCTGCTCCT	5817	MDSseq_474_449_F_R	CACCATCAGGATTTCTTACG	5849
515	A	MDSseq_235_515_A_F	CAGCCATCATCTCTTGCCCT	5818	MDSseq_235_515_A_R	ATTACTCGATGCAACAGCCC	5850
515	A	MDSseq_236_515_A_F	TGGACCTGGCGTTCTTTATC	5819	MDSseq_236_515_A_R	CAGGAGCAACACAATTCCT	5851
515	A	MDSseq_237_515_A_F	CGTAGTTTCTGTAACCAATTCA	5820	MDSseq_237_515_A_R	TTGGAGATCTTGTTCAGGGC	5852
515	A	MDSseq_239_515_A_F	GGCCATCGTCTTTTGTCATCT	5821	MDSseq_239_515_A_R	GCGTCAGAGATGAAGCAAGT	5853
515	A	MDSseq_263_515_A_F	CTGCTGTGTGTTCCGAGATG	5822	MDSseq_263_515_A_R	GTTGTGAGAGAGCCAGAAAT	5854
515	A	MDSseq_265_515_A_F	GGCCATCGTCTTTTGTCATCT	5823	MDSseq_265_515_A_R	GCGTCAGAGATGAAGCAAGT	5855
570	C	MDSseq_266_570_C_F	TTGATTGTGTTGCGCTTCTT	5824	MDSseq_266_570_C_R	GCATGAGCTCTGGAATCAGG	5856
570	F	MDSseq_268_570_F_F	CACCTGATTATTTTCCCTCA	5857	MDSseq_268_570_F_R	AACCTCCCTTAACTCAGTC	5889
570	I	MDSseq_270_570_I_F	CTGAGTGAGCGGAGGTGTTT	5858	MDSseq_270_570_I_R	TTGGCAATTTCTTTCATCAG	5890
570	J	MDSseq_271_570_J_F	CAGACAGCCCACTCCACG	5859	MDSseq_271_570_J_R	CCAAGACTTTGCAATCTCCA	5891
570	I	MDSseq_294_570_I_F	GCTGGCACTGGTGTCTATCA	5860	MDSseq_294_570_I_R	CCACGTAGGAATGAGAGCTGT	5892
581	E	MDSseq_277_581_E_F	GGGAGATTGTAGAGGTACAGC	5861	MDSseq_277_581_E_R	TAGCCAGGCGTGTGTA	5893
581	F	MDSseq_345_581_F_F	CCTTCTGAGTAGCTGGGCTC	5862	MDSseq_345_581_F_R	TAGACTTCTGACGCTGGGCT	5894
698	B	MDSseq_274_698_B_F	TGTCCTGAGCATCACAGTT	5863	MDSseq_274_698_B_R	CGGCTAAGTCTTTTCATCAGC	5895
698	E	MDSseq_275_698_E_F	GTAAGCATTTGTGTGCGAGC	5864	MDSseq_275_698_E_R	TGCCAAGGGCTGTTTCTAAT	5896
698	H	MDSseq_280_698_H_F	TGTGTACAGATTGCCCTACCC	5865	MDSseq_280_698_H_R	TGACGAATATACAGGATGAAAGTC	5897
698	I	MDSseq_287_698_I_F	GACAGCGCCTCTGGGTATTA	5866	MDSseq_287_698_I_R	TGAACAGAGCCACAGAGAAGTTT	5898
702	C	MDSseq_111_702_C_F	GTGATGAGGACAAGCTCGG	5867	MDSseq_111_702_C_R	ACGTTCCACAGCGGACTCA	5899
702	D	MDSseq_112_702_D_F	CAACCGTGCCTGTCTGTAAT	5868	MDSseq_112_702_D_R	CGCTCCATGAATGTATACAA	5900
702	A	MDSseq_113_702_A_F	TTCCACACACTCTCCTGC	5869	MDSseq_113_702_A_R	AAGGGTGGAGAGCCCTGAC	5901
702	B	MDSseq_114_702_B_F	CCCTCTGATCAGGCGACAGTC	5870	MDSseq_114_702_B_R	GGATATCTACAGCAGGCCCCA	5902
702	F	MDSseq_115_702_F_F	ACGCTTCTTGTGAGACCGAA	5871	MDSseq_115_702_F_R	AAGACGATCTTGTGTGCT	5903

702	I	MDSseq_116_702_I_F	AGCAGGGAGAGGTCATGTTG	<u>5872</u>	MDSseq_116_702_I_R	GGTGTGTGAGACTCACAGG	<u>5904</u>
702	I	MDSseq_117_702_I_F	CACTAGGGGACAGCTCCGT	<u>5873</u>	MDSseq_117_702_I_R	CTGCCATCTAGCACGAGCC	<u>5905</u>
702	B	MDSseq_178_702_B_F	AGGCACAGTCCCGTCTATG	<u>5874</u>	MDSseq_178_702_B_R	GAGAGCTCTGCTGCTGCT	<u>5906</u>
702	I	MDSseq_179_702_I_F	TCGTCAGTCAACACAGTCCC	<u>5875</u>	MDSseq_179_702_I_R	CCCACTGCAGTCTTGTC	<u>5907</u>
702	C	MDSseq_191_702_C_F	AGATCGGCCTAGTGGAAAT	<u>5876</u>	MDSseq_191_702_C_R	GCTCTCATTTCCCTCCTC	<u>5908</u>
702	I	MDSseq_196_702_I_F	CAGTCTTGTGCAAGCCCC	<u>5877</u>	MDSseq_196_702_I_R	CACAGTCTTGCCCTCTGTG	<u>5909</u>
702	I	MDSseq_269_702_I_F	AGCAGGGAGAGGTCATGTTG	<u>5878</u>	MDSseq_269_702_I_R	GGTGTGTGAGACTCACAGG	<u>5910</u>
722	F	MDSseq_63_722_F_F	TAAGTAGGTTGTGACCGGC	<u>5879</u>	MDSseq_63_722_F_R	CACTCTCCCAATCTCCCTGA	<u>5911</u>
722	C	MDSseq_132_722_C_F	ACCTGATAGGTTTCCCGGT	<u>5880</u>	MDSseq_132_722_C_R	ATACAGATGCCCTGGCTCG	<u>5912</u>
722	AA	MDSseq_135_722_AA_F	GACACGATCCTGGCTCTCG	<u>5881</u>	MDSseq_135_722_AA_R	GCCTGGGTGACACAGCTA	<u>5913</u>
722	B	MDSseq_141_722_B_F	TTCAGCCAGATCTGTTGTG	<u>5882</u>	MDSseq_141_722_B_R	GGGCTGGGAGTTACCTTAT	<u>5914</u>
722	B	MDSseq_146_722_B_F	TGCAACACACAGCAGTTTCAC	<u>5883</u>	MDSseq_146_722_B_R	ACCTCTACGGCAGGCTGAAT	<u>5915</u>
722	G	MDSseq_150_722_G_F	CAGTGTGCCGAGACATTGTT	<u>5884</u>	MDSseq_150_722_G_R	TGAGTCTCCACAAACATAGC	<u>5916</u>
722	A	MDSseq_441_722_A_F	TATTACCCAAAGCTGCACCC	<u>5885</u>	MDSseq_441_722_A_R	TCAAGACTCCCTGAGACCC	<u>5917</u>
751	U	MDSseq_455_751_U_F	AGACACTCTCCAGCTCTCGC	<u>5886</u>	MDSseq_455_751_U_R	GCAGGACCCCTGCACTACAGA	<u>5918</u>
751	W	MDSseq_456_751_W_F	CTCCAGGTAATGCGCTCAA	<u>5887</u>	MDSseq_455_751_W_R	TACTGTCTCTCATTTCCACAGC	<u>5919</u>
GenR2	F	MDSseq_420_GenR2_F_F	CCCAGGAGACAGAGGTTTCA	<u>5888</u>	MDSseq_420_GenR2_F_R	CCCAGACTGGCTTTGAACCTC	<u>5920</u>

Please replace Table 10 on pages 183-187 with the following table:

PLEASE SEE NEXT PAGE FOR TABLE

TABLE 10: SNPs

Gene	Exon	PMP Site	Location	Sequence	SEQ ID NO	PMP	AA change
214	B	1	3' UTR	CCTGTGCACTCTTGGGCATAGGCTAGGAGTGGAACTGCTG	5921	C>T	
214	C	-1	Intron	GGGCTCTGGCCACACTCAACGCAGGCGTTGTTCCGAGGA	5922	C>T	
214	E	+1	Intron	AAGACACATTTCTTATGAGCTGTAGTCACACAGTTTCATTAC	5923	T>C	
214	E	+2	Intron	CCCTGTGACCCCTCAACTCCCGGTCCCTCCAGCCCTGACAG	5924	G>C	
214	E	+3	Intron	CTCAACTCCCGGTCCCTC**CAGCCCTGACAGCCACTGTT	5925	**>TC	
214	E	-1	Intron	AGGCCGCTTCAACCCCTTCTCTCCGGCAGGGGCAATGGCCAA	5926	C>T	
214	E	1	Exon	CACCTGATTTCCCTCTCTCTGTGAGTGTCTGGGGCCCGTT	5927	G>T	Val > Leu
214	E	2	3' UTR	GGGCTCTGGCCACACTCAACGCAGGCGTTGTTCCGAGGA	5928	C>T	
214	E	3	3' UTR	TCAGGAGCCTGTGCTTGACCCGCCAATCCGCCCCCAACTC	5929	C>T	Pro > Ser
422	E	1	Exon	CAGACACATGACAACTGCTATGACCAGGCCAAGAGCTGGA	5930	T>C	
422	E	2	Exon	ACCCACACCTATTCACTGCTGCTCTGGCTCGGCATCAC	5931	G>A	
436	A	+1	Intron	GGCCGCGCGGGGGCGCGCGCGGTGCTGCCCTCGGCTCCGC	5932	G>T	
436	A	+2	Intron	CTGCTTGCTGCTGTTTAAAGCCACAGCCTGGGCCAGGCCG	5933	G>A	
436	A	-1	Intron	CCTTCCGGGGCATCATCCGCGATGACGGCGCCGCCAGCAGG	5934	G>T	
436	A	-2	Intron	GCCCTCCCCCGGGGGCCCGG*****CCCCGACCGGCCCGT	5935	*****>CCCCCGG G	
436	A	-3	Intron	TCCTCAAGGGMGAGGGCACTCCCCCCCCCGCGAGTTCCAT	5936	CC>***	
436	A	1	Exon	CGGGCGGGCGGGCCATGGCGGGCTGCTGCCCGCGCTGGCG	5937	G>T	Gly > Cys
436	A	2	Exon	TGAACCGCGCGCGTGCAACTGCTCATCTGGCCTACGTCATC	5938	C>T	Leu > Phe
436	C	+1	Intron	ATTCAGATGCGACCACTGTGTAAATCAGATGCCAGCTG	5939	G>A	
436	C	+2	Intron	AACGGTACGAGCTGTGGCCTCTGGGGAGGGGACGCCCTG	5940	T>C	
436	C	+3	Intron	TGTGGCCTCTGGGGAGGGCAGCCCCCTGAGCAGATCGCCCC	5941	A>G	
436	C	-1	Intron	CTCTCCGTGAGTCTCTGAGCGTGGCTTGCCCGTGTCT	5942	C>T	
436	D	-1	Intron	GTCACCTGTGTGTGGGGCGGGCCACGTGACACTTCTTTT	5943	G>A	
436	D	1	Exon	ATTCAGATGCGACCACTGTGTAAATCAGATGCCAGCTG	5944	G>A	
436	E	1	Exon	TGCGTAGCTTTCAACGGGTCTCGTCAAGACGTGTGAGGTGGC	5945	C>T	
436	G	1	Exon	TAGTGAGAGACGAGGACACAGTTTCCAGGACATGGCCGTG	5946	A>G	Ser > Gly
436	K	+1	Intron	GGGAGGCCCTTCTGCAGAGGCTGGCACCAGTGTGGCGTGT	5947	C>G	
436	K	+2	Intron	RCGACATCTCARGTTGGTGAATGATATGATGCTCTGAGAA	5948	T>A	
436	K	-1	Intron	GCTCACTCTCACCCATATGCTAAACTCAGGCGACCGTGTCTGT	5949	A>G	
436	K	-2	Intron	GATTCCAGGCTTCTCAGGAAAGGGGCGACGCAAAAGATTAAGAT	5950	G>C	

436	L	-1	Intron	CCAGGAGCGCACCTCCCTCCGCGCTGCCACAAGGGGTCCA	5951	C>T	
436	L	-2	Intron	GGTGAAGTCCCAAGAGCGCACCTCCCTCCGCGCTGCCACAA	5952	C>A	
436	L	-3	Intron	TGGCGTGGTGTCCCGTTAACCCGGGCGAGTCTGCCACTCT	5953	C>T	
436	L	1	3 UTR	AGCAGCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	5954	T>C	
454	B	-1	Intron	AAGTGCCTGCATCTCCAAAGCGGCTGCATCCCAACCCGCTGT	5955	C>T	
454	B	1	Exon	AGAGGTGAAGAGGAGATCGTGGAGAATGGAGTGAAGAAGT	5956	T>C	Val > Ala
454	E	-1	Intron	CTCCTGGAGAACGTCCTCTCGCGAGTTCCTTACATCTGTG	5957	C>T	
454	E	-2	Intron	CAAAGCCTAGTCTCTCGCCCGGGGTGAGTTAATGATGTC	5958	G>A	
454	E	1	Exon	CCCCTATAGGAATTGAGACCGGGAAGGTGTGTGTGTGTGTGAA	5959	G>A	Gly > Arg
454	E	2	Exon	AGACCGGAAGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG	5960	C>T	His > Tyr
454	E	3	Exon	TGTGAAGTCTGTGCGTGTGTGTGTGTGTGTGTGTGTGTGTG	5961	C>T	
454	F	+1	Intron	TCTACTGCTGAGTAATTAATTTATCCCAACCTCAGAAAGCT	5962	T>C	
454	F	-1	Intron	CATGGGCTCCCTCGGTCGCCAACCCTCAGTAAATGGCCATTTT	5963	A>C	
454	F	-2	Intron	GGCCCATGGGCTCCCTCGGTCGCCAACCCTCAGTAAATGGCCA	5964	C>T	
454	F	-3	Intron	TGTATCCATTTCTCTTTCATGATCCCAAGAACCAAGCCAAAG	5965	C>T	
454	G	-1	Intron	CACCTCTGGGAAAGAGACAGATCTGTGTGTGTGTGTGTGTGT	5966	A>T	
454	H	-1	Intron	GTTCTTCAATCAGCATTTTCTCTAAAAACCTTAAAGCAAT	5967	C>T	
454	H	-2	Intron	TTTAGGACATGAGTTTAAACGGTGATGTGTGTGTGTGTGTGTG	5968	G>A	
454	H	1	Exon	CCGTTGGTTCCATCAGTCCGCTGCCAATACAGTTTCCGTC	5969	G>A	Arg > His
454	H	2	Exon	CCGTCCCAATACAGTTTCCGCTGCCAATACAGTTTCCGTC	5970	G>A	Arg > His
454	K	1	Exon	GGAAACCAATGTTGAGAAAGGAGTCTGTGTGTGTGTGTGTGT	5971	G>A	Arg > Gln
454	L	-1	Intron	ATTTCACCTGAGTAACTCTGCCACTCTGTGTGTGTGTGTGTG	5972	C>T	
454	M	2	Exon	CATCGACTTCCTCATCGACAGTTACTCCAGTAACTGCTGTC	5973	C>G	Thr > Ser
454	M	+1	Intron	GTTCAACAGACACCAAGACAGGAGGAGATTCCATGAATCA	5974	C>T	
454	M	+2	Intron	GTAGTGAATACGTCGCTGGGCTCTACCCCGATCAACCACT	5975	C>T	
454	M	1	Exon	GCTGCAATTCCTCCCAAGGCGCTGTGTGTGTGTGTGTGTGT	5976	A>G	Thr > Ala
454	O	+1	Intron	CTCAGCTCTGTAATCCCAAGGCGCTGTGTGTGTGTGTGTGT	5977	G>A	
454	O	-1	Intron	ATAAATCATGTAATTAATTAATTAATTAATTAATTAATTAATTA	5978	T>C	
454	O	1	Exon	TGGACAACCAAGAGGAGATACAGCTGCTTAGAAAGGAGGCGA	5979	A>G	Gln > Arg
454	O	2	Exon	CCTAGATCCAGGAGATAGCCCGCTGTGTGTGTGTGTGTGTGT	5980	C>T	
454	O	3	Exon	GAGCCACAGGTGCTGCTGAGGAGCTGTGTGTGTGTGTGTGTG	5981	A>C	Glu > Ala
454	O	4	Exon	CTCTAACAGGAGCCCTGTGTGTGTGTGTGTGTGTGTGTGTGT	5982	G>T	
454	O	5	Exon	GGACATGGCTGACCTTGGCCATCTGCCAGCTGTGTGTGTGTGT	5983	T>A	
454	O	6	Exon	AGGATCCGGAAAGAGTTTCCAAAGAGTGAAGGGGAGTACAG	5984	A>G	Ile > Asn
515	A	1	Exon	CAGCGTGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG	5985	G>A	Arg > His
515	A	2	Exon	CGCTGCCTCCAGAGGAAGATGACAGGTGAGGCCAGATTAATAA	5986	G>A	Met > Ile
515	A	3	Exon	GGCGCTCCAGAGGCGTTAATGGCCAACTCCGGTGAAGCCATG	5987	G>C	MET > Ile

515	A	4	Exon	GTCAC	TGGACTCGGCCTAAGGTTTCTGGAACTTCCAGATT	5988	G>A	Val > Ile
515	A	5	Exon	ACTTC	CAGATTACAGAAATGTGATTTAGGAACTGTGGCA	5989	C>G	Ile > MET
515	A	6	3' UTR	CTTCC	AGATTACAGAAATGTGATTTAGGAACTGTGGCA	5990	T>C	
515	A	7	Exon	CTGGT	TGCAAGGTGTGACCAACAGGAATCCTGGAGGAACAGA	5991	A>G	
561	B	+1	Intron	TGTGT	GGGAGAGAAATGGCGTTGGCTGCCTGCAGGGGTG	5992	C>T	
561	B	+2	Intron	CGAGG	GTGCACAGGTGAATTCGGTTTGGTGACACCTGGC	5993	A>G	
561	B	1	Exon	AAGTT	CCGGCAGACCGCTGGCAGATTGACCTGTGGGTGG	5994	C>G	
561	C	1	Exon	GAATA	TATCCGCCCCCTCCGAGCCCTGGTGACAGGCCCGA	5995	G>A	
561	E	+1	Intron	CAGGG	CTCCCAACATACTCCGAGCCCTGGTGACAGGCCCGA	5996	T>C	
561	E	+2	Intron	ACTCC	GATAGTTACCAAGGTTTGGCCCTTTGACGACTGGAA	5997	G>C	
561	E	1	Exon	AGCTG	AGCTGAGCTGCCCTCAGCGCGGGGAAATACCTACGTCT	5998	C>T	Ala > Val
561	G	+2	Intron	GGGTG	GGGAGGGGTTTGTAGGGCCCTAACGACAGCGAGCGGC	5999	G>A	
561	G	+3	Intron	GTGGG	GAGGGTTTGTAGGGCCCTAACGACAGCGAGCGGC	6000	C>T	
561	G	-1	Intron	GCCAG	GGCTGGCTGTCCCTGAACGGCTCCGTTCCCTGTGCC	6001	G>A/C	
561	H	-1	Intron	GCTCA	CCCTCGGCGAGCCCGGAGCCAGCTCTGCTGTCCAC	6002	G>A	
561	H	-2	Intron	GGCTC	CCCATTTGCAAGACCGGGGGGCTCACCCTGGGCAGC	6003	G>*	
561	H	1	Exon	TCACC	CAGCCGATCTGCCACAGCCAGCGGACACCCCGGT	6004	A>G	
561	J	1	Exon	CTGGA	AGATGGGGGAGGAGGCGCGGCCAGCGGCACGTC	6005	G>A	
561	M	+1	Intron	AAAA	TAGTTAAGCGCAACCCCTATTGACACCTTCCCTGTGC	6006	C>A	
561	M	+2	Intron	TATGC	CAAGTCATGTAATGTTGACCAAGTATTTTCTTG	6007	G>A	
561	M	+3	Intron	GCCAA	AGTCATGTAATGTTGACCAAGTATTTTCTTG	6008	G>A	
561	M	+4	Intron	TTGGC	AAAAGCCACCTACGACCAAGAGCTGCCAGTAGTC	6009	G>A	
561	P	+1	Intron	TAAGC	AACCTATTAGCCCTTTTAATCTGTCCCGTTCT	6010	T>C	
561	P	1	Exon	GTGTT	TAGGGGAGCTGAATGGGAGAAAGGCTTGTGCC	6011	T>C	
561	X	-1	Intron	TCTGT	AGGGTAAGGAACACATCTGCTGTTACTACTTA	6012	A>T	
561	X	-2	Intron	TCTCT	GTGAGGGTAAGGAACACATCTGCTGTTACTACTTA	6013	A>C	
561	X	-3	Intron	GACAC	CCAGATTTTCAAGGATCAAGTTCTTCTTGCCCTAG	6014	T>A	
561	Y	+1	Intron	ATCTG	GGCCCTGGAGGAGCGGGCTGGGCCAGGGAGGAAC	6015	C>G	
561	Y	+2	Intron	TGAGG	CACCATGATCTCATCCACTATCTGCTGTTATCTGCTT	6016	C>T	
561	Y	+3	Intron	CCAGT	ATGATCTCATCCACTATCTGCTGTTATCTGCTT	6017	A>G	
561	Y	-1	Intron	TACCA	AGTCTCTAACAATGGGGGACCATCTACATGTCTCT	6018	G>C	
561	Y	-2	Intron	TCCAA	TGCGGAGAGTTCGTTGCTTTTATGACACACAGA	6019	G>A	
561	Y	-3	Intron	CTCCA	TATGGCGAGAGTTCGTTGCTTTTATGACACACAG	6020	C>T	
570	C	-1	Intron	TTAAC	CACTTACCGTAATGTTTTCATCTTGAAGACTG	6021	G>C	
570	C	1	Exon	TTAGG	TAAAGATCGAGGTCCGGAGAACCACTAGAGATTTT	6022	C>T	Pro > Leu
570	C	2	Exon	AGGCG	GCTTGCCTTTGTGTTCTTCTCTGTGGCAAGCGG	6023	T>C	Val > Ala
570	C	3	Exon	CTTTT	TGTGCTCTCTGTGGCAAGAGCGTTTTCATCACC	6024	G>A	Gly > Ser

570	C	4	Exon	GAGGGCAGTGCCTTCACAGACATGTTCAAGATACTGACGTA	6025	C>T	
570	F	+1	Intron	GTTGTGATTACAGAAATATAGTGTCTACACGACGTGTGCC	6026	T>C	
570	F	-1	Intron	AAGAAATCTTTCCAGGTCCGTTGTCTCTAACTGAAGAG	6027	C>T	
570	F	1	Exon	ATGTTCTTTGTCATGTGCTGGCCCTTTGCTGACAGGTAAAG	6028	G>A	
570	J	1	Exon	TATTTGAACATTAATCTTTTCTTCTGGCTGCTATTCAAG	6029	T>C	
581	F	+1	Intron	TGTGGCCACTTTGCTGTTCAGATTGTTGGCTTGGCTTGTT	6030	G>C	
581	F	+2	Intron	CTTTGCTGTTACAGATTGTTGGTTGGCTGTTATTCTG	6031	G>T	
581	F	-1	Intron	TGTACTATTGGCCTCAGGCCAATCCACACTCAGCCCCGAAA	6032	A>G	
698	B	-1	Intron	AGCCTTGCTATTGGCATCAGCTCTTTATTTTTTAAAAAT	6033	C>T	
698	B	1	Exon	CGGGGCCCTGGGGGGACACTGCCAGGGCCTGCCATGCTCAT	6034	G>A	
698	E	1	Exon	AGCCATGGGCATGCAAAATGAGAAAAAGCAATAATGTAAGTTA	6035	G>A	Arg > Lys
698	I	+1	Intron	GTCGCTCGCAAGGTTAGTCACCTGTGGGTTGCCATTCTA	6036	A>G	
698	I	+2	Intron	GTTATTGATGGGCCACACTTTGGGAAGACAGACAGTTG	6037	T>C	
698	I	-1	Intron	TGATGCTGATACGGGATCTGTGATCTGCTCCTCTGTG	6038	T>C	
702	A	-1	Intron	TTTATTAGACACTTTTCCGGGACGCTGCCAAGGGAAGAGAC	6039	G>A	
702	B	+1	Intron	ACCTGTCGTGAGGTGGGTGTGTGCCAGGGTGAAGAGCGCG	6040	T>C	
702	B	+2	Intron	GGAGGTGGGGCGGTGGCCAGGGTGAAGAAAGGGGCTCCGT	6041	G>C	
702	B	+3	Intron	GGGTGCGTGGCCAGGGGTGAGGAACAGGGTCTCCGTGAGGT	6042	G>C	
702	B	-2	Intron	GTGCCAGAGTCAGGGCTCCCAACCTTGGCGATGCTCGGAT	6043	A>G	
702	C	1	Exon	GCCCCACAGGCCACGACCCAGCGAGGTACGCCGGGGCCGAGC	6044	G>A	Ala > Thr
702	D	-1	Intron	GGGATGCCCTCGATGCCGGCTGCCGACAGAGGATTTCTGAGG	6045	G>A	
702	D	1	Exon	CCTCGTAGGGGAGCCCGTAGCGGACGGGTACCCACCCGGG	6046	C>T	Arg > His
702	F	-1	Intron	GCCCTGTCCCGGCTGCCACAGGGCCCGCTCCACGCCAC	6047	G>*	
702	F	1	Exon	GACGCGGTGGCCAGATCCGGGGTGAAGCTTTCTTCTCAA	6048	G>C	Arg > Pro
702	I	1	Exon	TGTGTGAGACTCACAGGCCGATGGATCTGTGGCTGCGGGC	6049	G>A	Asp > Asn
702	I	3	Exon	CCCAGAGGTGATGAGCAGAGCTCTGTAACCGTCTCTCCGAGC	6050	G>A	Val > Ile
722	AA	+2	Intron	CACGCAGTACAGATAATGCCATTCTAGTATACATCTGCCCTG	6051	A>G	
722	AA	-1	Intron	GGATGTCCTTTAATGTGGCAATATGAATAAACCATGCAATG	6052	A>G	
722	AA	-2	Intron	GCCACCACACCTGGCCAGGTGCTTTTATTTTAATGAAGGA	6053	C>T	
722	AA	-3	Intron	CTCAGGTGATCCATCCGCTGGGACTCCCAAGTGTGAGA	6054	C>G	
722	AA	-4	Intron	CTGACCTCAGGTGATCATCGGCTCGGACTCCCAAGTGC	6055	C>T	
722	C	1	Exon	GGTGGAGGAGATTAGAAACAGTATTGATAAATAACTCAAT	6056	G>C	Ser>Thr
722	F	+1	Intron	AAGTGAGTAATGGAGACTCCGCTTTGTTAAATCATGTTT	6057	G>A	
722	G	-1	Intron	AAAAATGCTAACACATATGATTGTAGTTGCTAATATATGTT	6058	T>C	
757	A	+1	Intron	ACTTTGTTTAGAGCCCTCCGTAATAATATACATCTGTAT	6059	G>C	
757	A	+2	Intron	GAGTTGCTTAAATAGACTCGGGCTTCACCAATAGTCTCT	6060	C>T	
757	A	+3	Intron	AGGCCAGCCCTCAGAAACCGTTTCTAGTGTACATTTTGTGG	6061	C>T	

757	A	+4	Intron	ACCAAGCCAATGTTATAGACGTTTGGACTGATTGTGAAA	6062	G>C	
757	A	+5	Intron	GACTGATTGTGGAAAGGAGGGGGGAAGAGAGAGGATC	6063	G>A	
757	A	+6	Intron	GCTAGTGTATTCTTCACAGTGCCAGGAAAGAGTGGTTT	6064	A>G	
757	A	-1	Intron	CCGAGCCGGGGCGCTGTGGCAGCGCTCGGGCCAGGCCGG	6065	G>A	
757	A	2	Exon	TTGCACGAGTTCGCCCGCTGGTGAGTACGGCTGCCACGG	6066	G>C	
757	A	4	Exon	CTCACCCTTCATCGACCCGGCCCGCTTCCGCTACCCCGA	6067	G>C	
757	A	5	Exon	AGCCGGAGAAACCGGCAGCGTGATCACCAGCGGTGGAT	6068	C>T	

Please replace Table 11A on pages 189-191 with the following table:

PLEASE SEE NEXT PAGE FOR TABLE

TABLE 11A: ASA PRIMERS

SNP	ASA Type	RFLP Enzyme	ASO Primer1	SEQ ID NO.	ASO Primer2	SEQ ID NO.	Base change	AA change
214_B_1	RFLP	NdeII					C>T	
214_C_1	ASO		ACCTCAACCCAGGCGTT	6069	CACCTCAACTCAGGCCGTTTG	6080	C>T	
214_E_+1	RFLP	PvuII					T>C	
214_E_+2	RFLP	MspI					G>C	
214_E_1	RFLP	AvaI					C>T	
214_E_1	ASO		CTCTCTCTGTGAGTGTCC	6070	CTCTCTCTTTGAGTGTCTGG	6081	G>T	Val>Leu
214_E_2	ASO		ACCTCAACCCAGGCGTTT	6071	CCACCTCAACTCAGGCCGTTT	6082	C>T	
214_E_3	ASO		TGCTTGACCCCAATCC	6072	GTGCTTGACCTCCAATCCG	6083	C>T	Pro>Ser
422_E_2	ASO		TCATACTCGTCTGGC	6073	TATTCATCTCATGCTCTGGCT	6084	G>A	
436_A_+2	ASO		TGTTTTAAAGCCACAGCCT	6074	CTGTTTTAAAGCCACAGCCTGG	6085	G>A	
436_A_1	ASO		CCCTCGGTTCCACCGTC	6075	GCCATGGCGTGTGCTGC	6086	G>T	Gly>Cys
436_A_2	ASO		GTGCAACTGCTCATCTGTG	6076	CGTGCAACTGTTCATCTCTGG	6087	C>T	Leu>Phe
436_C_+1	RFLP	DraIII					G>A	
436_C_1	RFLP	MwoI					C>T	
436_D_1	RFLP	DraIII					G>A	
436_E_1	RFLP	AvaiI					C>T	
436_G_1	ASO		GCAGGACACAGTTTCCAGGA	6077	CAGGACACGGTTTCCAG	6088	A>G	Ser>Gly
436_K_+1	RFLP	AlwNI					C>G	
436_K_2	ASO		CTCAGGAAGGGGACACGCA	6078	CTCAGGAACGGGGACACGCA	6089	G>C	
436_L_1	ASO		CTCCCTCCCGCGCTGCAC	6079	CTCCCTCCTGCGCTGCCAC	6090	C>T	
436_L_3	RFLP	XmaI					C>T	
436_L_1	RFLP	HhaI					T>C	
454_B_1	RFLP	BstUI					T>C	Val>Ala
454_E_1	RFLP	PstI					C>T	
454_E_1	RFLP	HpaII					G>A	Gly>Arg
454_E_2	RFLP	NlaIII					C>T	His>Tyr
454_E_3	RFLP	BanI					C>T	
454_F_2	ASO		CCCTCGGTCGCCACCCGTC	6091	CCCTCGGTTCCACCCGTC	6107	C>T	
454_G_1	RFLP	BstYI					A>T	
454_H_1	ASO		CATCACTGCCGTCGCAAA	6092	CCATCACTGCCCATCCCAAT	6108	G>A	Arg>His
454_H_2	ASO		CAGTTTCGCTGCGCTTGA	6093	CAGTTTCATCGCCTTGACG	6109	G>A	Arg>His
454_K_1	RFLP	AlwNI					G>A	Arg>Gln

454_L_-1	RFLP	EarI					C>T	
454_M_+1	ASO		CCAAGACACGGAGAGATT	6094	ACCAAGACATGAGAGATTCC	6110	C>T	
454_M_1	RFLP	MspAI				6110	C>T	
454_M_2	ASO		CATCGACACTTACTCCAG	6095	CATCGACAGTTACTCCAG	6111	A>G	Ala>Thr
454_O_1	RFLP	PvuII				6111	C>G	Thr>Ser
454_O_3	RFLP	HhaI					A>G	Gln>Arg
454_O_5	ASO		ACTTTGCCATCCTGCCAG	6096	ACTTTGCCAACCTGCCAG	6112	A>C	Glu>Ala
454_O_6	RFLP	MboII				6112	T>A	Ile>Asn
515_A_1	ASO		GCGGATCCGCATCTTCT	6097	TGCGGATCCACATCTTCTGG	6113	A>G	
515_A_2	ASO		GGAAGATGACAGGTGAGC	6098	AGGAAGATTAACAGGTGAGCC	6114	G>A	Arg>His
515_A_3	RFLP	HaeIII				6114	G>A	MET>Ile
515_A_4	RFLP	Bsu36I					G>C	MET>Ile
515_A_5	RFLP	BsmI					G>A	Val>Ile
515_A_6	RFLP	BsmI					C>G	
515_A_7	RFLP	XcmI					T>C	Ile>MET
561_B_+1	ASO		AGAAATGGCCGTTGGCTG	6099	GAGAATGGCTGTTGGCTGC	6115	A>G	
561_B_1	ASO		CACGCTGGCAAGATTGAC	6100	CACGCTGGCAAGATTGAC	6115	C>T	
561_C_1	RFLP	MwoI				6116	C>G	
561_E_+1	RFLP	MspI					G>A	
561_E_1	ASO		CCTCACGGCGGGGAAAT	6101	CCCTCACGGGTGGGAAATAC	6117	T>C	
561_H_1	ASO		CATCCTGCCACAGCCACAG	6102	ATCCTGCCGACGCCACA	6118	C>T	Ala>Val
561_J_1	ASO		GGAAGGAGGGCGGCCA	6103	GGGAAGGAGACGGGCCAG	6118	A>G	
561_M_+1	ASO		CGCAAAACCCCTATTGAC	6104	GGCAAAACCACTATTGACC	6119	G>A	
561_P_1	ASO		GAGCTGAACGGGCAGAA	6105	GGAGCTGAATGGGCAGAAAG	6120	C>A	
561_X_-3	ASO		ATTTTCAGGCAATCAAGTTCTTC	6106	ATTTTCAGGCAACAAGTTCTTCT	6121	T>C	Arg>Trp
561_Y_+1	RFLP	BsrBI				6122	T>A	
561_Y_-1	RFLP	Fnu4HI					C>G	
570_C_1	RFLP	MspI					G>C	
570_C_2	ASO		GCTTTTGTGCTCTTCTCTG	6123	CTTTTGTGGCTTCTCTCT	6135	C>T	Pro>Leu
570_C_3	ASO		CTTTCACAGACATGTTCAAG	6124	GCCTTTCACAGATAAGTTCAAGA	6136	T>C	Val>Ala
570_C_4	RFLP	AflIII				6136	G>A	Gly>Ser
570_F_1	RFLP	DdeI					C>T	
581_F_+2	ASO		AGATTGTTTCGGTTTGCTT	6125	TCAGATTGTTCTGTTTGCTTG	6137	G>A	
698_E_1	ASO		CATGCAAAATGAGAAAAGCAAT	6126	GGCATGCAAAATGAAAAAGCAAT	6138	G>T	
698_L_+1	ASO		CCCCACAGGTGACTTAACCTT	6127	CCCACAGGGCGACTAACCC	6139	G>A	Arg>Lys
702_A_-1	ASO		ACTTTTCCGGCAGCTGC	6128	ACTTTTCCGTCAGCTGCCCC	6140	A>G	
702_B_+1	ASO		AGGTGGGTGTGTGGCCAG	6129	GGTGGGTGTGCTGGCCA	6141	G>A	
						6141	T>C	

702_B_+3	ASO		AGGGTGAGGAACGGGGT	6130	AGGGTGAGCAACGGGGT	6142	G>C	
702_C_1	RFLP	HaeII					G>A	Ala>Thr
702_D_1	RFLP	HhaI					C>T	Arg>His
702_F_1	RFLP	NciI					G>C	Arg>Pro
702_I_1	RFLP	XcmI					G>A	Asp>Asn
702_I_3	RFLP	DpnII					G>A	Val>Ile
722_C_1	ASO		GATTAGAAACAGTATTGATAAA	6131	GATTAGAAACACTATTGATAAA	6143	G>C	Ser>Thr
722_F_+1	RFLP	Tth111					G>A	
722_G_-1	ASO		AACAACATATGATTGATTTGCTA	6132	CAACTATGACTGTAGTTGC	6144	T>C	
757_A_+4	RFLP	HpyCH4IV					G>C	
757_A_-1	ASO		GCTGTGCGCAGCGCTC	6133	CGCTGTGCACAGCGCTCG	6145	G>A	
757_A_2	ASO		GCGCCGCTGGTGGAGTA	6134	GCGCCGCTCGTGGAGTA	6146	G>C	
757_A_4	RFLP	Sau96I					G>C	
757_A_5	RFLP	Cac8I					C>T	

Please replace Table 11B on page 194 with the following table:

TABLE 11B: EPA PRIMERS

SNP	Primer Seq. (5'-3')	SEQ ID NO:
436_K_-2	TTATTCTTTGCGTGCCC	<u>6147</u>
436_K_-2	ACCTTCCCTTCTCCAAGACC	<u>6148</u>
436_K_-2	ATTCCAGGCTTCTCAGGAA	<u>6149</u>
436_K_-2	CGCCTGAGTTTAGCATAGGG	<u>6150</u>
454_F_-2	CATGGGCTCCCTCGGT	<u>6151</u>
454_F_-2	CCGGGGAAGTCGATATTGTT	<u>6152</u>
454_F_-2	CATGGGCTCCCTCGGT	<u>6153</u>
570_C_2	GCGGTCTTGCTTTTGTGG	<u>6154</u>
570_C_2	TTACTCTGGCGCTCTCCACT	<u>6155</u>
570_C_2	CGGTCTTGCTTTTGTGG	<u>6156</u>
698_I_+1	AGAATGGCAACCCACAGG	<u>6157</u>
698_I_+1	GCTGGTTCTCACGCTGCATATT	<u>6158</u>
698_I_+1	GTAGAATGGCAACCCACAGG	<u>6159</u>